

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:28:58 ; Search time 75 Seconds

(without alignments)
614.730 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853

Sequence: 1 MINGSCCRIGDTISQVMP.....ANSFOSQSDGQMDPHVEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
A_Geneseq.101002:*
1: /SID2/gcgdata/geneseq-emb1/AA1980.DAT:*
2: /SID2/gcgdata/geneseq-emb1/AA1981.DAT:*
3: /SID2/gcgdata/geneseq-emb1/AA1982.DAT:*
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22: /SID2/gcgdata/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	100.0	346	22	ABBA4522
2	1853	100.0	346	22	AAU06197
3	1853	100.0	346	22	AAU04373
4	1853	100.0	346	22	AAU04373
5	1853	100.0	346	22	AAU04373
6	1853	100.0	346	22	AAU04373
7	1853	100.0	346	22	AAU04373
8	1853	100.0	346	22	AAU04373
9	1853	100.0	346	22	AAU04373
10	1853	100.0	346	22	AAU04373

11	1839	99.2	346	22	ABBA4523	Human GPCR1a polyp
12	1570	84.7	296	22	AAU06197	Human GPCR1a polyp
13	897.5	48.4	387	22	AAU077992	Human GPCR1a polyp
14	883.5	47.7	363	20	AAU04373	Human GPCR1a polyp
15	883.5	47.7	363	22	AAU04373	Human GPCR1a polyp
16	881.5	47.6	387	21	AAU06197	Human GPCR1a polyp
17	880.5	47.5	387	21	AAU06197	Human GPCR1a polyp
18	880.5	47.5	387	21	AAU06197	Human GPCR1a polyp
19	879.5	47.5	363	23	AAU077993	Human GPCR1a polyp
20	879.5	47.5	363	23	AAU077993	Human GPCR1a polyp
21	529	28.5	384	23	AAU04373	Human GPCR1a polyp
22	529	28.5	423	20	AAU04373	Human GPCR1a polyp
23	529	28.5	423	22	AAU04373	Human GPCR1a polyp
24	529	28.5	423	22	AAU04373	Human GPCR1a polyp
25	529	28.5	423	22	AAU04373	Human GPCR1a polyp
26	510	27.5	476	20	AAU04373	Human GPCR1a polyp
27	451.5	24.4	319	21	AAU04373	Human GPCR1a polyp
28	450.5	24.3	319	23	AAU04373	Human GPCR1a polyp
29	448.5	24.2	319	21	AAU04373	Human GPCR1a polyp
30	448.5	24.2	319	21	AAU04373	Human GPCR1a polyp
31	448.5	24.2	319	22	AAU04373	Human GPCR1a polyp
32	366.5	19.8	330	23	AAU04373	Human GPCR1a polyp
33	366.5	19.8	341	22	AAU04373	Human GPCR1a polyp
34	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
35	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
36	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
37	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
38	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
39	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
40	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
41	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
42	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
43	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
44	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp
45	366.5	19.8	346	22	AAU04373	Human GPCR1a polyp

ALIGNMENTS

RESULT 1	ABBA4522	ABBA4522 standard; Protein: 346 AA.
ID	ABBA4522	
AC	ABBA4522	
XX	28-JAN-2002 (first entry)	
DE	Human GPCR1a polypeptide SEQ ID NO. 2.	
XX	Human; GPCR1; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytosolic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV.	
OS	Homo sapiens.	
XX	WO200174904-A2.	
XX	11-OCT-2001.	
XX	30-MAR-2001; 2001WO-US10241.	
XX	31-MAR-2000; 2000US-193664P.	
XX	05-APR-2000; 2000US-194614P.	
XX	06-APR-2000; 2000US-195063P.	
XX	06-APR-2000; 2000US-195066P.	
XX	06-APR-2000; 2000US-195067P.	
XX	06-APR-2000; 2000US-195068P.	
XX	06-APR-2000; 2000US-195069P.	
XX	06-APR-2000; 2000US-195070P.	
XX	06-APR-2000; 2000US-195510P.	

PR 21-JUL-2000; 2000US-219855P.
 PR 27-JUL-2000; 2000US-221284P.
 PR 28-JUL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-082317Z.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spederna SK;
 PI Padigaru M, Mishnu VS, Tchernev VT, Sylek KA, Li L;
 PI Baumgartner JC, Gusev VY;
 XX
 DR WPI: 2001-639351/73.
 DR N-PSDB; ABA81529, ABA81530.
 XX
 PS New human G-protein coupled receptor X, GPCR, polypeptide useful in
 PT treatment or prevention of GPCR associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically.
 XX
 PS Claim 1; Page 8; 157Pp; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA81529-ABA81532) that
 CC encode G-coupled protein-receptor related polypeptides
 CC (AB44522-AB44543). The isolated polypeptide having a sequence differing
 CC by no more than 15 % of amino acid residues from one of 22 amino acid
 CC sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCR) polypeptides. The polypeptides have potential cardiac,
 CC antihypertensive, anabolic, cytostatic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC hematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.
 XX
 SQ Sequence 346 AA:
 Query Match 100.0%; Score 1853; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1, se-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MNGSCCRLEGSTISVMPPLIVAFVGLGALNGVALGCFCHMTKRPSTYLLFNLA 60
 QY 1 MNGSCCRLEGSTISVMPPLIVAFVGLGALNGVALGCFCHMTKRPSTYLLFNLA 60
 Db 1 MNGSCCRLEGSTISVMPPLIVAFVGLGALNGVALGCFCHMTKRPSTYLLFNLA 60
 QY 61 DFLMCLCPFRDYLRHHMAFGDIPCRVGLFTLAMNAGSIVLTVAAADRYKVVHP 120
 Db 61 DFLMCLCPFRDYLRHHMAFGDIPCRVGLFTLAMNAGSIVLTVAAADRYKVVHP 120
 QY 121 HHAVENTISTRVAGIVCTLMALVILGTYYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 Db 121 HHAVENTISTRVAGIVCTLMALVILGTYYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 QY 181 FOLEFMPRLGILFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPSVSAR 240
 Db 181 FOLEFMPRLGILFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPSVSAR 240

Db 181 FOLEFMPRLGILFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHTLSFTYNSMMDPLVYFSSPFPKFNKLKISLKRK 300
 Db 241 LYFLMTVPSSACDPVSHGALHTLSFTYNSMMDPLVYFSSPFPKFNKLKISLKRK 300
 QY 301 QPGHKTQREMPISNLTGRSCISVANSFOSOSDQMPHIVEMH 346
 Db 301 QPGHKTQREMPISNLTGRSCISVANSFOSOSDQMPHIVEMH 346
 RESULT 2
 AAU06197
 ID AAU06197 standard; Protein; 346 AA.
 XX
 AC AAU06197;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE Novel human G protein-coupled receptor (GPCR) protein.
 XX
 KM Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
 KM hyperproliferative disorder; neurological disorder; psychiatric disease;
 KM inflammatory disorder; respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200173029-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-0509522.
 XX
 PR 27-MAR-2000; 2000US-192419P.
 PR 06-SEP-2000; 2000US-230459P.
 PR 20-SEP-2000; 2000US-0666535.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Ye J, Cravchik A, Di Francesco V, Beasley EM;
 XX
 DR WPI: 2001-616503/71.
 DR N-PSDB; AAS12581.
 XX
 PT Novel human G-protein coupled receptor proteins and nucleic acid
 PT molecules encoding the protein for use in developing human therapeutics
 PT and diagnostic compositions and for identifying modulators of the
 PT protein -
 XX
 PS Claim 1; Fig 1; 66pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC coupled receptor (GPCR) which is related to the chemokine receptor
 CC subfamily. The cDNA and gene sequences encoding for GPCR are also
 CC given in the invention. The sequences of the invention are useful
 CC for diagnosing and treating diseases or conditions mediated by human
 CC proteases. Such diseases include hyperproliferative disorders
 CC (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease),
 CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders
 CC (e.g. diabetes) and respiratory disorders (e.g. adult respiratory
 CC distress syndrome, ARDS). The GPCR protein is also useful for identifying
 CC a modulator of the expression of the protein. It also serves as a target
 CC for identifying agents for use in mammalian therapeutic applications,
 CC e.g. a human drug, particularly modulating a biological or pathological
 CC response in a cell or tissue that expresses the protein, in biological
 CC assays related to GPCRs that are related to members of the chemokine
 CC receptor subfamily, in drug screening assays and in competition binding
 CC assays. GPCR is also useful in diagnosing a disease or predisposition to
 CC a disease mediated by the peptide, in pharmacogenomic analysis. The
 CC polynucleotide sequences can also be used in gene therapy. The present
 CC sequence represents the novel human GPCR of the invention.

SQ Sequence 346 AA:
 Query Match 100.0%; Score 1853; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIYAFVIGALNGVALCGCFCHMKTKWPTVYLFNLAVA 60
 DB 1 MYNSCCRIEGDTISQVMPPLIYAFVIGALNGVALCGCFCHMKTKWPTVYLFNLAVA 60
 QY 61 DFLMTCLEPFRIDYLRRRHMAFGDIPCRVGLFTLAMNRAAGIYFLVVAADRFEKVVHP 120
 DB 61 DFLMTCLEPFRIDYLRRRHMAFGDIPCRVGLFTLAMNRAAGIYFLVVAADRFEKVVHP 120
 QY 121 HHAVNTISTRVAAGIVCTLMALVILGTYYLLLENHLCVQETAVSCESFIMESANGMHDIM 180
 DB 121 HHAVNTISTRVAAGIVCTLMALVILGTYYLLLENHLCVQETAVSCESFIMESANGMHDIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 3
 AA004373 standard; Protein: 346 AA.
 ID AA004373:
 AC AA004373:
 XX 23-OCT-2001 (first entry)
 DT
 XX Human G-protein coupled receptor, hRUP19.
 DE
 XX Human G-protein coupled receptor; GPCR; hRUP19; agonist;
 KW Inverse agonist; Lung cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200136471-A2.
 PD
 XX 25-MAY-2001.
 PF 16-NOV-2000; 2000MO-US31509.
 XX
 XX 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Chen R, Dang HT, Lowitz KP.
 XX
 DR WPI: 2001-355616/37.
 DR N-PSDB; AAS07946.
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 PS Claim 45; page 110-111; 160pp; English.

The sequence represents a human G-protein coupled receptor (GPCR),
 hRUP19. The endogenous and non-endogenous, constitutively activated
 versions of human G-protein coupled receptors (GPCR), are useful for
 direct identification of candidate compounds as receptor agonists,
 CC direct agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. Lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

SQ Sequence 346 AA:
 Query Match 100.0%; Score 1853; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDTISQVMPPLIYAFVIGALNGVALCGCFCHMKTKWPTVYLFNLAVA 60
 DB 1 MYNSCCRIEGDTISQVMPPLIYAFVIGALNGVALCGCFCHMKTKWPTVYLFNLAVA 60
 QY 61 DFLMTCLEPFRIDYLRRRHMAFGDIPCRVGLFTLAMNRAAGIYFLVVAADRFEKVVHP 120
 DB 61 DFLMTCLEPFRIDYLRRRHMAFGDIPCRVGLFTLAMNRAAGIYFLVVAADRFEKVVHP 120
 QY 121 HHAVNTISTRVAAGIYCTLMALVILGTYYLLLENHLCVQETAVSCESFIMESANGMHDIM 180
 DB 121 HHAVNTISTRVAAGIYCTLMALVILGTYYLLLENHLCVQETAVSCESFIMESANGMHDIM 180
 QY 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 DB 181 FOLEFFMPLGIILFCSEFKIWSLRROQLARQARKKATRFIMVAIVETICYLPSVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSTFTYNSMLDPLVYFSSPSPKRYNKLKICSLKPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEWH 346

RESULT 4
 AAG80968 standard; Protein: 346 AA.
 ID AAG80968:
 AC AAG80968:
 XX 28-AUG-2001 (first entry)
 DT
 XX Human nGPCR11 #2.
 DE
 XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;

KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KM neuroprotective.
 XX Homo sapiens.
 OS
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31581.
 XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogel I G, Wood LS, Parodi IA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kayles PS, Bannigan CM, Ruff V, Sejltz T, Huff RM;
 XX
 DR WPI: 2001-389826/41.
 DR N-PSDB: AAH51008.
 XX
 PT New G protein-coupled receptor (GPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 XX
 PS Claim 37; Page 89; 261pp; English.

The present invention relates to novel G protein-coupled receptors (GPCRs) where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The GPCR coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCR are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCR in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCR activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD, (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.

Sequence 346 AA:

Query Match 100.0%; Score 1853; DB 22; Length 346;

Best Local Similarity 100.0%; Pred. No. 1.5e-199; Indels 0; Gaps 0;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MYNGSCRIEGRDITISQVMPPLITVAFVIGALNGVALGCFCEPHMTKWTQSTVYLENLAVA 60
 QY 61 DFLIMTCLPFRDIYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTYVAADRYFKVYHP 120

DB 61 DFLIMTCLPFRDIYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTYVAADRYFKVYHP 120
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 DB 121 HHAVENTSTRVAAGIYCTMALVYILGTVYLLLENHLCVETAVSCSEPTMESANWHIM 180
 QY 181 FOLEFMPILGILFCSEKIVMSLRRROQLARQARKKATRFIMVVAIVITCYLPSVSR 240
 DB 181 FOLEFMPILGILFCSEKIVMSLRRROQLARQARKKATRFIMVVAIVITCYLPSVSR 240
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 DB 241 LYFLMTVPSSACDPVHGALHTLSTPTNMSMLDPLVYFSSPEPKFYNKLTCSLKP 300
 QY 301 QPESHKTQREEMPIISNLGRSCISVANSFQSDQSDQMPHIVEH 346
 DB 301 QPESHKTQREEMPIISNLGRSCISVANSFQSDQSDQMPHIVEH 346
 RESULT 5
 AAE24354
 ID AAE24354 standard; Protein; 346 AA.
 XX
 AC AAE24354;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human G protein coupled receptor (GPCR), 57242 protein.
 XX
 XX Human: G protein coupled receptor; GPCR; 57242 protein; overweight;
 KW metabolic disorder; lipogenesis; lipolysis; immunomodulator; heart;
 KW bone disorder; osteoporosis; osteogenesis; bone resorption; cachexia;
 KW hyperlipidaemia; anorexia; haematopoietic disorder; osteopathic;
 KW autoimmune disorder; psoriasis; multiple sclerosis; brain disorder;
 KW degenerative disease; Alzheimer's disease; Pick disease; diabetes;
 KW adipocyte; hyperplastic growth; hypertrophic growth; gene therapy;
 KW obesity; anorectic; receptor.
 KW
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..37
 FT /label= Signal_peptide
 FT Protein 38..346
 FT /note= "Human mature GPCR protein"
 FT Domain 1..20
 FT /note= "N-terminal non-transmembrane domain"
 FT Modified-site 3..6
 FT /note= "N-glycosylation site"
 FT Cleavage-site 9..10
 FT /note= "Cleavage site for mitochondrial preseq"
 FT Domain 21..42
 FT /note= "Transmembrane domain"
 FT Domain 32..278
 FT /note= "GPCR domain"
 FT Domain 43..51
 FT /note= "Non-transmembrane domain"
 FT Domain 52..70
 FT /note= "Transmembrane domain"
 FT Region 71..89
 FT /note= "Extracellular loop"
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 FT /note= "Nuclear localisation signal"
 FT Domain 90..111
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 FT Domain 112..130
 FT /note= "Non-transmembrane domain"
 FT Domain 131..152
 FT /note= "Transmembrane domain"
 FT Region 153..184
 FT /note= "Extracellular loop"
 FT Domain 185..201

```

FT      /note= "Transmembrane domain"
FT      202..220
FT      /note= "Non-transmembrane domain"
FT      Peptide
FT      204..220
FT      /note= "Nuclear localisation signal"
FT      Modified-site
FT      216..219
FT      /note= "cAMP- and cGMP-dependent protein kinase
FT      phosphorylation site"
FT      Domain
FT      221..245
FT      /note= "Transmembrane domain"
FT      Region
FT      245..258
FT      /note= "Extracellular loop"
FT      Domain
FT      246..255
FT      /note= "Non-transmembrane domain"
FT      Domain
FT      259..280
FT      /note= "Transmembrane domain"
FT      Domain
FT      281..346
FT      /note= "C-terminal cytoplasmic domain"

PN      WO200218579-A2.
PN      07-MAR-2002.
PD
XX      29-AUG-2001; 2001WO-US26882.
XX      29-AUG-2000; 2000US-228409P.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Glucksmann MA:
XX      WPI: 2002-479433/51.
XX      N-PSDB: AAD39181.
XX
XX      Human G protein coupled receptor nucleic acid and polypeptide
XX      molecules, designated 57242, useful for diagnosing, preventing or
XX      treating aberrant lipogenesis or aberrant lipolysis, obesity, diabetes
XX      or bone disorders (e.g. osteoporosis)
XX
XX      Claim 9; Page 112-113; 114pp; English.
XX
XX      The invention relates to G protein coupled receptor (GPCR) family
XX      member, 57242 and its corresponding nucleic acid sequence. The 57242
XX      nucleic acid and polypeptide are useful for diagnosing, preventing
XX      or treating a subject having or at risk of developing a metabolic
XX      disorder, particularly a disorder associated with aberrant lipogenesis
XX      or aberrant lipolysis, obesity or diabetes. The 57242 DNA and protein
XX      are also useful for treating a subject having bone disorder, where
XX      the disorder is osteoporosis or a disorder associated with aberrant
XX      osteogenesis or aberrant bone resorption. These diseases include
XX      obesity, diabetes, hyperlipidaemia, overweight, anorexia or cachexia.
XX      The 57242 DNA and protein are also useful for treating a subject
XX      having haematopoietic disorders, autoimmune disorders e.g. psoriasis
XX      and multiple sclerosis, brain disorders, degenerative diseases e.g.
XX      Alzheimer's disease and Pick disease and disorders involving heart.
XX      The 57242 nucleic acid and polypeptide are also useful for modulating
XX      adipocyte activity such as hyperplastic growth, hypertrophic growth
XX      or lipogenesis. The 57242 DNA is used in gene therapy. The present
XX      sequence is human 57242 protein.
XX
SQ      Sequence      346 AA:

```

```

Query Match      100.0%; Score 1853; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 1,5e-199;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MYNSCCRIEEDTISQVAPLLIYAFVYLGALGNCVALGCGCFHKTKKPSVTYILEFNLA 60
QY      1 MYNSCCRIEEDTISQVAPLLIYAFVYLGALGNCVALGCGCFHKTKKPSVTYILEFNLA 60
Db      1 MYNSCCRIEEDTISQVAPLLIYAFVYLGALGNCVALGCGCFHKTKKPSVTYILEFNLA 60
QY      61 DFLIMTCLPRTDYLYLRRRRHAFGDIQCVGLFTLANNRAGSIVFLTVVAADRYFKVYHP 120
QY      61 DFLIMTCLPRTDYLYLRRRRHAFGDIQCVGLFTLANNRAGSIVFLTVVAADRYFKVYHP 120
Db      61 DFLIMTCLPRTDYLYLRRRRHAFGDIQCVGLFTLANNRAGSIVFLTVVAADRYFKVYHP 120

```

```

QY      121 HHAVENTISTVAAGIYCTIMALVILGTVYLLENHLCVOETAVSCSEFTMESANGNHDIM 180
QY      121 HHAVENTISTVAAGIYCTIMALVILGTVYLLENHLCVOETAVSCSEFTMESANGNHDIM 180
Db      121 HHAVENTISTVAAGIYCTIMALVILGTVYLLENHLCVOETAVSCSEFTMESANGNHDIM 180
QY      181 FOLEFFMPGLIIFCSPKTIWSSLRRROQLARQRMKKAFTIMVAIVETITCPLPSVSAR 240
QY      181 FOLEFFMPGLIIFCSPKTIWSSLRRROQLARQRMKKAFTIMVAIVETITCPLPSVSAR 240
Db      181 FOLEFFMPGLIIFCSPKTIWSSLRRROQLARQRMKKAFTIMVAIVETITCPLPSVSAR 240
QY      241 LYFLMTVPSSACDPSVGHALHITLSTFYNNMSMDPLVYFFSSPFPKFNKIKTCSLKP 300
QY      241 LYFLMTVPSSACDPSVGHALHITLSTFYNNMSMDPLVYFFSSPFPKFNKIKTCSLKP 300
Db      241 LYFLMTVPSSACDPSVGHALHITLSTFYNNMSMDPLVYFFSSPFPKFNKIKTCSLKP 300
QY      301 QPQHSKTQREPEMPSINLGRSCISVANSFOSQSDQMPDHVEWH 346
QY      301 QPQHSKTQREPEMPSINLGRSCISVANSFOSQSDQMPDHVEWH 346
Db      301 QPQHSKTQREPEMPSINLGRSCISVANSFOSQSDQMPDHVEWH 346

RESULT 6
AA014788
ID      AA014788 standard; Protein; 346 AA.
AC
XX      AA014788;
XX
DT      28-JUN-2002 (first entry)
XX
DE      Human purinergic-like G-protein coupled receptor (AXOR87).
XX
KW      Human; purinergic-like G-protein coupled receptor; AXOR87; immunity;
KW      autoimmunity; inflammation; immunodeficiency; bacterial infection;
KW      fungal infection; viral infection; protozoa infection; cancer; diabetes;
KW      obesity; anorexia; bulimia; asthma; psoriasis; rheumatoid arthritis;
KW      osteoarthritis; psychotic disorder; neurological disorder; vaccine;
KW      chromosome 12q24.
XX
OS      Homo sapiens.
XX
PN      GB2365868-A.
PD
XX      27-FEB-2002.
XX
PF      25-MAY-2001; 2001GB-0012860.
PR      30-MAY-2000; 2000US-0580675.
PR      02-NOV-2000; 2000GB-0026839.
XX
XX      (SMK ) SMITHKLINE BEECHAM CORP.
XX      (SMK ) SMITHKLINE BEECHAM PLC.
XX      (GLAX ) GLAXO GROUP LTD.
XX
PI      Ignar DM, Elshourbagy N, Gattu M, Shabon U;
XX
WPI: 2002-364852/40.
N-PSDB: AAL42499.
XX
XX      New purinergic-like G-protein coupled receptor AXOR87 polypeptide and
XX      polynucleotide, useful for treating diseases related to autoimmunity,
XX      inflammation, immunodeficiency, or bacterial, fungal, viral and
XX      protozoal infections
XX
XX      Claim 2; Page 36; 47pp; English.
XX
XX      The invention comprises the amino acid and coding sequence of the human
XX      purinergic-like G-protein coupled receptor AXOR87. The AXOR87 DNA and
XX      protein sequences of the invention may be used for treating diseases
XX      related to immunity, autoimmunity, inflammation, immunodeficiency, and
XX      infections (i.e. bacterial, fungal, viral, protozoan). The AXOR87 DNA and
XX      protein sequences are particularly useful for treating: cancers,
XX      diabetes, obesity, anorexia, bulimia, asthma, psoriasis, rheumatoid
XX      arthritis, osteoarthritis, as well as psychotic and neurological
XX      disorders. The AXOR87 DNA and protein sequences may also be used as
XX      vaccines. The present amino acid sequence (encoded by a sequence located
XX      on chromosome 12q24) represents the human AXOR87 protein.

```

XX Sequence 346 AA; 100.0%; Score 1853; DB 23; Length 346;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMKTKPSTVYLEFLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMKTKPSTVYLEFLAVA 60
 QY 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 DB 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 QY 121 HHAVENTSTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAVENTSTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIILFCSEFKIYWSLRRROQLARQARKKATRFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIILFCSEFKIYWSLRRROQLARQARKKATRFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGMDPHIVEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGMDPHIVEMH 346

RESULT 7
 ABB08596
 ID ABB08596 standard; Protein; 346 AA.
 AC ABB08596;
 DT 01-JUL-2002 (first entry)
 DE Human lipocyte-originated G protein-coupled receptor protein TGR13.
 KW Antinflammatory; anorectic; obesity; inflammation; gene therapy;
 KW human; G protein-coupled receptor protein TGR13.
 OS Homo sapiens.
 PN WO200202767-A1.
 PD 10-JAN-2002.
 PE 02-JUL-2001; 2001WO-JP05711.
 PR 04-JUL-2000; 2000JP-0206860.
 PR 31-JUL-2000; 2000JP-0235274.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;
 DR WPI; 2002-164535/21.
 DR N-PSDB; ABA99236.
 PT New human lipocyte-originated G protein-coupled receptor proteins TGR13
 PT and encoding DNAs, for developing drugs to treat obesity and
 PT inflammation, including gene therapy
 PS Claim 1; Fig 2; 101pp; Japanese.
 CC This invention relates to a human lipocyte-originated G protein-coupled
 CC receptor proteins TGR13, thought to be antinflammatory and anorectic in
 CC their action. The proteins and encoded DNAs are for use in developing
 CC drugs to treat obesity and inflammation, including gene therapy.

CC The present sequence represents the human lipocyte-originated G
 CC protein-coupled receptor protein TGR13.
 XX Sequence 346 AA; 100.0%; Score 1853; DB 23; Length 346;
 Query Match Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMKTKPSTVYLEFLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIVAFVIGALGNGVALCGFCFHKMKTKPSTVYLEFLAVA 60
 QY 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 DB 61 DFLMICLPFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIYFLTVAAADRYEKVHP 120
 QY 121 HHAVENTSTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAVENTSTRVAGIVCTLMALVILGTVYLLLENHLCVQETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIILFCSEFKIYWSLRRROQLARQARKKATRFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIILFCSEFKIYWSLRRROQLARQARKKATRFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMLDPLVYFSSPSFPKFNKLIKICSLPK 300
 QY 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGMDPHIVEMH 346
 DB 301 QPGHSKTQRPPEMPISNLGRSCISVANSFOSQSDGMDPHIVEMH 346

RESULT 8
 AAE16172
 ID AAE16172 standard; Protein; 346 AA.
 AC AAE16172;
 DT 26-MAR-2002 (first entry)
 DE Human G-protein coupled receptor 3 (GCRHC-3) protein.
 KW Human; G-protein coupled receptor 3; cell proliferative disorder;
 KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
 KW gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
 KW acquired immune deficiency syndrome; inflammatory disorder; infection;
 KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
 KW diabetes; obesity; osteoporosis; gene therapy; GCRHC-3.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FH Peptide 1..32
 FT /label= Signal_peptide
 FT 33..346
 FT Protein
 FT /label= Human_mature_GCRHC-3_Protein
 FT 20..44
 FT Domain
 FT /note= "Transmembrane domain"
 FT 93..110
 FT Domain
 FT /note= "Transmembrane domain"
 FT 137..154
 FT Domain
 FT /note= "Transmembrane domain"
 FT 222..244
 FT Domain
 FT /note= "Transmembrane domain"
 PN WO200187937-A2.
 XX 22-NOV-2001.
 PD

PF 17-MAY-2001; 2001WO-US16285.
 XX
 PR 18-MAY-2000; 2000US-205628P.
 PR 22-MAY-2000; 2000US-206222P.
 PR 25-MAY-2000; 2000US-207566P.
 PR 02-JUN-2000; 2000US-208834P.
 PR 02-JUN-2000; 2000US-208861P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;
 PI Khan FA, Gandhi AR, Walia NK, Nguyen DB, Yue H, Hafalia A;
 PI Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;
 XX
 DR WPI: 2002-089844/12.
 DR N-PSDB; AAD26371.
 XX
 PT Novel G-protein coupled receptors and polynucleotides useful for
 PT diagnosis, treatment and prevention of disorders of cell proliferation,
 PT neurological, cardiovascular, metabolic disorders and viral infections
 PT
 XX
 PS Claim 1; Page 105-106; 115pp; English.
 XX
 CC The invention relates to human G-protein coupled receptor (GPCR)
 CC polypeptides and polynucleotides. GPCR polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in
 CC the diagnosis, prevention and treatment of disorders which include
 CC cell proliferative disorders such as arteriosclerosis, hepatitis,
 CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukemia,
 CC lymphoma; neurological disorders such as epilepsy, ischemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxia, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
 CC hypertension, vascular tumours, myocardial infarction, hypertensive
 CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis;
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and
 CC viral infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
 CC are useful as probes for assessing toxicity of test compounds. They are
 CC also used in gene therapy. The present sequence is human G-protein
 CC coupled receptor 3 (GCR3-3) protein.
 CC
 XX
 SQ Sequence 346 AA;
 Query Match 100.0%; Score 1853; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1.5e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYNGSCRIEPTISQVPLIIVAFVIGALGVGALGFCFHMKTWKSTYTLNLA 60
 DB 1 MYNGSCRIEPTISQVPLIIVAFVIGALGVGALGFCFHMKTWKSTYTLNLA 60
 QY 61 DFLMLICLFFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIVELTVAADRFFK 120
 DB 61 DFLMLICLFFRDYLLRRHMAFGDIPCRVGLFTLAMNAGSIVELTVAADRFFK 120
 QY 121 HHAVENTISRVAGVCTMAVYIGTYVLLLENHLQVETAVSCSEFMSANQWHDIM 180
 DB 121 HHAVENTISRVAGVCTMAVYIGTYVLLLENHLQVETAVSCSEFMSANQWHDIM 180
 QY 181 PLEFFMPGLIIFCSFKIWSILRRQOLARQARKKATRTIMVAIVETITCLPSV 240
 DB 181 PLEFFMPGLIIFCSFKIWSILRRQOLARQARKKATRTIMVAIVETITCLPSV 240

DB 181 PLEFFMPGLIIFCSFKIWSILRRQOLARQARKKATRTIMVAIVETITCLPSV 240
 QY 241 LVELMTVPSSACDPVSHGALHITISPTYNNSMLDPLVYFESSPPKPKFNKIKISLMPK 300
 DB 241 LVELMTVPSSACDPVSHGALHITISPTYNNSMLDPLVYFESSPPKPKFNKIKISLMPK 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFQSDGQMDPHIVEMH 346
 RESULT 9
 ID AAU11401 standard; Protein; 346 AA.
 AC AAU11401;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE HM74-like G-protein coupled receptor (GPCR).
 XX
 KW HM74-like GPCR: G-protein coupled receptor; antibacterial; fungicide;
 KW protozoacide; analgesic; cytotatic; neuroleptic; nootropic;
 KW anticonvulsant; tranquiliser; viral infection; pain; cancer; anorexia;
 KW bulimia; asthma; central nervous system disease; CNS disease;
 KW cardiovascular disease; hypotension; hypertension; angina pectoris;
 KW myocardial infarction; urinary retention; osteoporosis; ulcer; asthma;
 KW inflammatory disorder; benign prostatic hypertrophy; multiple sclerosis;
 KW psychotic disorder; neurological disorder; dyskinesia;
 KW Huntington's disease; Tourette's syndrome; anxiety; schizophrenia;
 KW manic depression; delirium; dementia; mental retardation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Domain 20..37
 FT /label= Transmembrane_domain_1
 FT Domain 53..73
 FT /label= Transmembrane_domain_2
 FT Domain 91..113
 FT /label= Transmembrane_domain_3
 FT Domain 133..150
 FT /label= Transmembrane_domain_4
 FT Domain 180..197
 FT /label= Transmembrane_domain_5
 FT Domain 223..242
 FT /label= Transmembrane_domain_6
 FT Domain 260..279
 FT /label= Transmembrane_domain_7
 FT Region 101..118
 FT /label= GPCR-region
 FT /note= "G-protein coupled receptor region"
 XX
 PN WO200177320-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-EP03811.
 XX
 PR 05-APR-2000; 2000US-194701P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Xiao Y;
 XX
 DR WPI: 2002-049147/06.
 DR N-PSDB; AAS18501.
 XX
 PT Novel isolated polynucleotide, useful for treating infection, pain,
 PT cancer, asthma, hypertension, myocardial infarction, urinary retention,
 PT osteoporosis, encodes the human HM74-like G-protein coupled receptor
 PT polypeptide -
 XX

PS Claim 1; Fig 2; 77pp; English.

XX The invention describes a novel isolated polynucleotide (I) encoding a
CC human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents
CC that regulate HM74-like GPCR are useful for modulating the activity of
CC the protein in a disease selected from bacterial, fungal, protozoan, and
CC viral infection, pain, cancer, anorexia, bulimia, asthma, central nervous
CC system (CNS) disease, cardiovascular disease, hypotension, hypertension,
CC angina pectoris, myocardial infarction, urinary retention, osteoporosis,
CC ulcer, asthma, inflammation, allergy, benign prostatic hyper trophy,
CC multiple sclerosis and dyskinesia such as Huntington's disease and
CC Tourette's syndrome. The composition is also useful for treating
CC psychotic and neurological disorders such as anxiety, schizophrenia,
CC manic depression, delirium, dementia and severe mental retardation. (I)
CC or the HM74-like GPCR polypeptide are also useful for treating the above
CC mentioned diseases. (I) is useful in a diagnostic assay for detecting
CC diseases, susceptibility to diseases and abnormalities related to the
CC presence of mutations in the nucleic acid sequences which encode a GPCR.
CC The polypeptide is useful to identify test compounds which may act as
CC agonists or antagonists at the receptor site and which can be regulated
CC to provide therapeutic effects. The polypeptide is also useful as a bait
CC protein in a two-hybrid or three-hybrid assay, and to immunise a mammal
CC for production of polyclonal antibodies. This the amino acid sequence of
CC human HM74-like GPCR described in the method of the invention.

XX Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 23; Length 346;

Best Local Similarity 100.0%; Pred. No. 1.5e-199; Mismatches 0; Gaps 0;

Matches 346; Conservative 0; Indels 0; Gaps 0;

QY 1 MYNGSCRIEGLDTSQVMPPLIYFAVLGALNGVALGCFEHHKTKMPTVYLENLAVA 60
DB 1 MYNGSCRIEGLDTSQVMPPLIYFAVLGALNGVALGCFEHHKTKMPTVYLENLAVA 60
QY 61 DFLMILCEPRTDYLLRRRHHAFGDIPIRCVGLFTLAMNRAISYFLTVVADRFKXVHP 120
DB 61 DFLMILCEPRTDYLLRRRHHAFGDIPIRCVGLFTLAMNRAISYFLTVVADRFKXVHP 120
QY 121 HNAVNTISTRVAGIVCTLMALVILGTVYLLLENHLQVETAVSCSEFIMESANGMDIM 180
DB 121 HNAVNTISTRVAGIVCTLMALVILGTVYLLLENHLQVETAVSCSEFIMESANGMDIM 180
QY 181 FOLEFPMPLGILLFCSEFIKWSLRRROQLARQARKKATRFIMVAIVFICYLPVSAR 240
DB 181 FOLEFPMPLGILLFCSEFIKWSLRRROQLARQARKKATRFIMVAIVFICYLPVSAR 240
QY 241 LFLMTVTVSSACDDPSVHGALHTLSTFTYMNMSMLDPLVYFSSPPKRYNKLKICSLPK 300
DB 241 LFLMTVTVSSACDDPSVHGALHTLSTFTYMNMSMLDPLVYFSSPPKRYNKLKICSLPK 300
QY 301 QGHSKTORPEEMPIISNLGRSCISVANSFQSDGQMDPHIVEMH 346
DB 301 QGHSKTORPEEMPIISNLGRSCISVANSFQSDGQMDPHIVEMH 346

RESULT 10

AAEI7077
ID AAEI7077 standard; Protein: 346 AA.

XX AAEI7077;

DT 18-APR-2002 (first entry)

DE Human G-protein coupled receptor (GPCRx14) protein.

XX Human: G-protein coupled receptor: GPCRx14; cerebroprotective; vomiting;
KW receptor-mediated disorder: therapy; urinary retention; allergy; obesity;
KW osteoporosis; angina pectoris; restenosis; atherosclerosis; hypotension;
KW anorexia; tumour; migraine; acute heart failure; ulcer; antiinflammatory;
KW stroke; hypertension; neuronal disorder; myocardial infarction psychotic;
KW depression; mental retardation; neurodegenerative disease; antibacterial;
KW Alzheimer's disease; dementia; ischaemia; Parkinson's disease; antiviral;

KW Huntington's disease; anxiety; antifungal; immunosuppressive; cytostatic;
KW vulnerable; analgesic; anorectic; anabolic; diuretic; cardiac; nootropic;
KW antileptic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.

OS Homo sapiens.

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Location/Qualifiers

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

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/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

/note="Transmembrane domain"

Disclosure: Page 29; 46pp; English.

The present invention relates to a G-protein coupled receptor (GPCR) and nucleotide encoding it. GPCR are useful in the manufacture of a medicament for the prevention and/or treatment of receptor-mediated disorders e.g. viral infections, virus and bacterial diseases, diseases and disorders involving disturbances of cell migration, diseases or perturbations of immune system including cancers, development of tumours and tumour metastasis, inflammatory and neoplastic processes, bacterial and fungal infections, in wound and bone healing, dysfunction of CC regulatory growth functions; pains, diabetes, obesity, anorexia, bulimia, urinary retention, osteoporosis, angina pectoris, atherosclerosis, restenosis, diseases involving excessive or reduced proliferation or loss of smooth muscle cells, aneurysm, stroke, ischaemia, ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting; blood circulating CC affections including acute heart failure, hypotension, hypertension and myocardial infarction psychotic; neuronal disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, severe mental retardation; degenerative diseases; neurodegenerative diseases such as Alzheimer's disease, Parkinson's disease; and dyskinesias e.g. Huntington's disease or Gilles de la Tourette's syndrome and other CC related diseases. The present sequence is GPCRx14 protein.

Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 23; Length 346;

Best Local Similarity 100.0%; Pred. No. 1.5e-199; Mismatches 0; Gaps 0;

Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIIAFLVIGALNGVALCGFCFHKMTKPKSTVYLLENLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIAFLVIGALNGVALCGFCFHKMTKPKSTVYLLENLAVA 60
 QY 61 DELLMLICLPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFTLVVADRFEKVHP 120
 DB 61 DELLMLICLPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFTLVVADRFEKVHP 120
 QY 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIIFCSEFIVMSLRROQLARQARMKATREFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIIFCSEFIVMSLRROQLARQARMKATREFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMDPLVYSSPSFPEFYKTKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMDPLVYSSPSFPEFYKTKICSLKPK 300
 QY 301 QPGHSTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346
 DB 301 QPGHSTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346

RESULT 11
 ABB44523
 ID ABB44523 standard; Protein: 346 AA.
 AC ABB44523;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human GPCR1c polypeptide SEQ ID NO 5.
 XX
 KW Human: GPCR, G-coupled protein-receptor; cardiant; antiarteriosclerotic;
 KW anabolic; cytosolic; antiviral; gene therapy; cardiomyopathy; obesity;
 KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
 KW infection; human immunodeficiency virus; HIV.
 XX
 OS Homo sapiens.
 XX
 PN WO200174904-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10241.
 XX
 PR 31-MAR-2000; 2000US-193664P.
 PR 05-APR-2000; 2000US-194614P.
 PR 06-APR-2000; 2000US-195063P.
 PR 06-APR-2000; 2000US-195066P.
 PR 06-APR-2000; 2000US-195067P.
 PR 06-APR-2000; 2000US-195068P.
 PR 06-APR-2000; 2000US-195069P.
 PR 06-APR-2000; 2000US-195070P.
 PR 21-JUL-2000; 2000US-219855P.
 PR 27-JUL-2000; 2000US-221284P.
 PR 28-JUL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-0823172.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
 PI Padigaru M, Mishu VS, Tchernev VT, Spytek KA, Li L;

PI Baumgartner JC, Gusev VY;
 XX WPI: 2001-639351/73.
 DR N-PSDB; ABA81531.
 XX
 XX New human G-protein coupled receptor X, GPCR-X, polypeptide useful in
 PT treatment or prevention of GPCR-X associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically
 XX
 PS Claim 1; Page 11; 157pp; English.

The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 encode G-coupled protein-receptor related polypeptides
 (ABB44522-ABB44543). The isolated polypeptide having a sequence differing
 by no more than 15 % of amino acid residues from one of 22 amino acid
 sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCR-X) polypeptides. The polypeptides have potential cardiant,
 CC antiarteriosclerotic, anabolic, cytosolic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCR-X-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC haematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide expression in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.

Sequence 346 AA:
 SQ

Query Match 99.2%; Score 1839; DB 22; Length 346;
 Best Local Similarity 99.4%; Pred. No. 5.6e-198;
 Matches 344; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MYNSCCRIEEDTISQVMPPLIIAFLVIGALNGVALCGFCFHKMTKPKSTVYLLENLAVA 60
 DB 1 MYNSCCRIEEDTISQVMPPLIIAFLVIGALNGVALCGFCFHKMTKPKSTVYLLENLAVA 60
 QY 61 DELLMLICLPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFTLVVADRFEKVHP 120
 DB 61 DELLMLICLPFRDYLLRRRHHAFGDIICRGVGLFTLAMNRAGSIVFTLVVADRFEKVHP 120
 QY 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 DB 121 HHAANTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGWHDIM 180
 QY 181 FOLEFEMPLGIIIFCSEFIVMSLRROQLARQARMKATREFIMVVAIVFTTCYLPVSAR 240
 DB 181 FOLEFEMPLGIIIFCSEFIVMSLRROQLARQARMKATREFIMVVAIVFTTCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMDPLVYSSPSFPEFYKTKICSLKPK 300
 DB 241 LYFLMTVPSSACDPSVHGALHITLSFTYMSMDPLVYSSPSFPEFYKTKICSLKPK 300
 QY 301 QPGHSTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346
 DB 301 QPGHSTQRPPEMPISNLGRRSCISVANSFOSQSDGQMDPHIYEMH 346

RESULT 12
 AAG80934
 ID AAG80934 standard; Protein: 296 AA.

XX AAG80934;
 AC
 XX 28-AUG-2001 (first entry)
 DT
 XX Human nGPCR11 #1.
 DE
 XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 XX signal transduction; schizophrenia; thyroid disorder; renal failure;
 XX rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 XX cardiovascular disease; proliferative disorder; hormonal disorder;
 XX neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 XX attention deficit-hyperactivity disorder/attention deficit disorder;
 XX Parkinson's disease; migraine; senile dementia; inflammatory disease;
 XX rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 XX neuroprotective.
 OS Homo sapiens.
 XX WO200136473-A2.
 PN
 XX 25-MAY-2001.
 PD
 XX 16-NOV-2000; 2000WO-US31581.
 PF
 XX 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PANA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogeli G, Wood LS, Parodi IA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kayles PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
 XX WPI: 2001-389826/41.
 XX N-PSDB; AAH50974.
 DR
 XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 PS Claim 37; Pages 77-78; 261pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is one such G protein-coupled receptor. GPCRs are also known as
 CC seven transmembrane receptors and function in signal transduction. The
 CC nGPCR coding sequences are useful for screening a human to diagnose a
 CC disorder affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease.
 XX
 XX Sequence 296 AA:
 SQ
 Query Match 84.7%; Score 1570; DB 22; Length 296;
 Best Local Similarity 100.0%; Pred. No. 8.2e-168;
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21 LLVAVPLGALGNGVALGCGFPMKTKWPSYVLLFNLAVADFLMCLPFRDYLLRRH 80
 DB 1 LLVAVPLGALGNGVALGCGFPMKTKWPSYVLLFNLAVADFLMCLPFRDYLLRRH 60
 OY 81 WAFGDIPCRYGFTLLAMNRAGSIVFLVVAADRYFKVPHHNAVNTISFVAGIVCTLM 140
 DB 61 WAFGDIPCRYGFTLLAMNRAGSIVFLVVAADRYFKVPHHNAVNTISFVAGIVCTLM 120
 OY 141 ALVILGTVYLLLENHLCVQETAVSCSFIMESANGHNDIMFQLEFPMPIGILLFCSFKIV 200
 DB 121 ALVILGTVYLLLENHLCVQETAVSCSFIMESANGHNDIMFQLEFPMPIGILLFCSFKIV 180
 OY 201 WSLRRQQLARQARMKKATPEIMVAIVFTCYLPSVARSALYFLMTVPSSACDPVHGAL 260
 DB 181 WSLRRQQLARQARMKKATPEIMVAIVFTCYLPSVARSALYFLMTVPSSACDPVHGAL 240
 OY 261 HTPLSFTYNSMDPLVYFSSPSPFKFYNNKIKICSLKPKQPKSHKTQRPDEMPIS 316
 DB 241 HTPLSFTYNSMDPLVYFSSPSPFKFYNNKIKICSLKPKQPKSHKTQRPDEMPIS 296
 RESULT 13
 AAU77992 standard; Protein; 387 AA.
 XX
 XX AAU77992:
 XX 02-JUL-2002 (first entry)
 XX
 XX Human Inflammation-associated GPCR EX20 polypeptide. ;
 XX
 XX Human: Inflammation-associated G-protein coupled receptor; GPCR; EX20;
 XX inflammatory disease; asthma; adult respiratory distress syndrome; ARDS;
 XX chronic obstructive pulmonary disease; COPD; bronchitis; emphysema;
 XX pneumoconiosis; neutrophil; eosinophil related disorder; allergy;
 XX lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;
 XX ulcerative colitis; skin disease; eczematous dermatitis; receptor.
 XX
 OS Homo sapiens.
 XX
 XX WO200213845-A2.
 XX 21-FEB-2002.
 XX
 PF 16-AUG-2001; 2001WO-EP09466.
 XX
 PR 18-AUG-2000; 2000US-0641653.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PI Jaraal G, Yousefi S;
 XX WPI: 2002-329542/36.
 XX N-PSDB; ABK47759.
 DR
 XX
 PT New pharmaceutical composition comprising EX20 polypeptide, EX20
 PT polynucleotide, antibodies against EX20 polypeptide, antisense
 PT oligonucleotides against EX20 polynucleotide, useful for treating
 PT inflammatory disease -
 XX
 PS Claim 2; Page 31-32; 36pp; English.
 XX
 CC The present invention relates to human inflammation-associated

CC G-protein coupled receptor (GPCR) EX20 polypeptide and the
 CC polynucleotide sequence encoding it. A pharmaceutical composition
 CC comprising EX20 polypeptide, a variant of EX20, an antibody which
 CC immunoreacts with EX20, a polynucleotide encoding EX20 or an antisense
 CC oligonucleotide comprising a nucleotide sequence complementary to
 CC EX20 can be used in diagnostic and therapeutic applications for
 CC treating an inflammatory disease. Such inflammatory diseases include
 CC asthma, adult respiratory distress syndrome (ARDS), chronic obstructive
 CC pulmonary disease (COPD) including chronic bronchitis, emphysema,
 CC pneumoconiosis, neutrophil or eosinophil related disorders, airway and
 CC lung-related disorders, rheumatoid arthritis, inflammatory bowel
 CC disease, ulcerative colitis, and skin diseases such as eczematous
 CC dermatitis. The present sequence represents human inflammation-associated
 CC GPCR EX20 polypeptide.
 CC
 XX Sequence 387 AA;
 SQ
 Query Match 48.4%; Score 897.5; DB 23; Length 387;
 Best Local Similarity 52.8%; Pred. No. 5.3e-92;
 Matches 180; Conservative 50; Mismatches 104; Indels 7; Gaps 4;
 QY 5 SCRRIGDTISQVMPPLIIVAFVIGALNGVALGCGFHHKTKRPSVYLFNLAVADFL 64
 Db 17 NCCVFRDDEIVAVLPVGLGFIIGLNGGLAMIFCFHLKSKSSRIFFNLAVADFL 76
 QY 65 MCLPFTDYLLRRRMAFGDIPCRVGLFTLAMNRAGSIVELTVVADRYFKVYVPHNAV 124
 Db 77 IICLPFYMDYVRRSDMKFGDIPCRILVFMFAMNRQSSIIFFLVVANDRFRVYVPHNAL 136
 QY 125 NTISTRVAAGICTMALVILGTVYLLLENHLCOVETAVSCSEFTMESANGMHDIMFOLE 184
 Db 137 NKISMTAAITISCLLMGITGLVHLKRLKLLONGTANVCISFSICHPFRMHAMFLE 196
 QY 185 FFMPLGILFCSEFKIYWSLRROQLARQAKKATRFIMVAIVITTCYLPVSARLYFL 244
 Db 197 FELPLGILFCSARIITWSLRQ-OMDRNAKIKRAITFTIMVAIVITTCYLPVSARLYFL 255
 QY 245 WTVPSA--CD--PSVGHALHITLSTFTYMSMLDPLVYFSSPFPKFNKLCISLKP 299
 Db 256 WLLHTSGTGNCEYVSDLAFFITLSTFTYMSMLDPLVYFSSPFPFNFTSLINCLOR 315
 QY 300 KOPGHSKTORPEMPISNLGRSCISVANSFQSGQMDP 340
 Db 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPALMANSGEPWSP 355
 RESULT 14
 AAM94654
 ID AAM94654 standard; Protein; 363 AA.
 XX
 AC AAM94654;
 XX
 DT 29-APR-1999 (first entry)
 XX
 DE G-protein coupled receptor HM74A protein.
 XX
 KW HM74A receptor; G-protein coupled receptor; infection; pain; cancer;
 KW diabetes; obesity; neurological disorder; heart failure; hypertension;
 KW asthma; allergy.
 XX
 OS Homo sapiens.
 PN
 AC WO9856820-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12386.
 XX
 PR 12-JUN-1997; 97US-0049480.
 XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 XX
 PI Bergsma DJ, Elshourbagy NA, Guerrero SF, Li X, Mooney JL;

XX
 DR WPI: 1999-095273/08.
 DR N-PSDB: AAX16671.
 XX
 PR New isolated G-protein coupled receptor, HM74A - used to develop
 PR products for treating e.g. infections, pain, cancers, diabetes,
 PR obesity, neurological disorders, heart failure, hypertension, asthma
 PR or allergies
 XX
 PS Claim 1; Page 31-32; 40pp; English.
 XX
 CC The present sequence is a member of the G-protein coupled receptor
 CC (7TM receptor) family, designated the HM74A receptor. The proteins,
 CC agonists, antagonists and polynucleotides can be used for treating
 CC disorders associated with increased or reduced expression or activity
 CC of HM74A, e.g. bacterial, fungal, protozoan and viral infections,
 CC particularly infections caused by HIV-1 or HIV-2, pain, cancers,
 CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease,
 CC acute heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
 CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
 CC psychotic and neurological disorders, including anxiety, schizophrenia,
 CC manic depression, depression, delirium, dementia, and severe mental
 CC retardation, and dyskinesias such as Huntington's disease or
 CC Gilles de la Tourette's syndrome. The products can also be used for
 CC detection, diagnosis and drug screening.
 CC
 XX Sequence 363 AA;
 SQ
 Query Match 47.7%; Score 883.5; DB 20; Length 363;
 Best Local Similarity 52.8%; Pred. No. 1.8e-90;
 Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;
 QY 5 SCRRIGDTISQVMPPLIIVAFVIGALNGVALGCGFHHKTKRPSVYLFNLAVADFL 64
 Db 17 NCCVFRDDEIVAVLPVGLGFIIGLNGGLAMIFCFHLKSKSSRIFFNLAVADFL 76
 QY 65 MCLPFTDYLLRRRMAFGDIPCRVGLFTLAMNRAGSIVELTVVADRYFKVYVPHNAV 124
 Db 77 IICLPFYMDYVRRSDMKFGDIPCRILVFMFAMNRQSSIIFFLVVANDRFRVYVPHNAL 136
 QY 125 NTISTRVAAGICTMALVILGTVYLLLENHLCOVETAVSCSEFTMESANGMHDIMFOLE 184
 Db 137 NKISMTAAITISCLLMGITGLVHLKRLKLLONGTANVCISFSICHPFRMHAMFLE 196
 QY 185 FFMPLGILFCSEFKIYWSLRROQLARQAKKATRFIMVAIVITTCYLPVSARLYFL 244
 Db 197 FELPLGILFCSARIITWSLRQ-OMDRNAKIKRAITFTIMVAIVITTCYLPVSARLYFL 255
 QY 245 WTVPSA--CD--PSVGHALHITLSTFTYMSMLDPLVYFSSPFPKFNKLCISLKP 299
 Db 256 WLLHTSGTGNCEYVSDLAFFITLSTFTYMSMLDPLVYFSSPFPFNFTSLINCLOR 315
 QY 300 KOPGHSKTORPEMPISNLGRSCISVANSFQSGQMDP 340
 Db 316 KMTGEPDNNRSTSVELTGDPNKT-RGAPALMANSGEPWSP 355
 RESULT 15
 AA004379
 ID AA004379 standard; Protein; 363 AA.
 XX
 AC AA004379;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human G-protein coupled receptor, hrUP25.
 XX
 KW Human; G-protein coupled receptor; GPCR; hrUP25; agonist;
 KW inverse agonist; lung cancer.
 XX
 OS Homo sapiens.
 XX

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:36:29 ; Search time 29 Seconds
(without alignments)
351.046 Million cell updates/sec

Title: US-09-942-374-2
Perfect score: 1953
Sequence: 1 MYNSGCCRIEGRISQVMP.....ANSFQSQSDGQMPHIVEMH 346

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCRU8.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	28.5	423	2	US-08-955-713-2
2	510	27.5	476	2	US-08-955-713-4
3	451.5	24.4	319	3	US-09-130-749-2
4	451.5	24.4	319	3	US-09-130-749-2
5	371	20.0	362	3	US-08-513-974B-374
6	362.5	19.6	373	2	US-08-558-524A-4
7	362.5	19.6	373	3	US-08-749-707-4
8	346.5	18.7	370	3	US-08-781-250-2
9	336	18.1	339	2	US-08-153-848-4
10	336	18.1	339	2	US-08-812-871-3
11	336	18.1	339	2	US-09-298-843A-44
12	336	18.1	339	4	US-09-088-337B-44
13	336	18.1	339	5	PCT-US93-11153-44
14	336	18.1	339	5	PCT-US95-07180-2
15	328.5	17.7	302	2	US-08-467-948A-30
16	328.5	17.7	302	2	US-08-467-947A-30
17	327	17.6	309	4	US-09-422-869-20
18	325	17.5	344	2	US-08-467-948A-8
19	325	17.5	344	2	US-08-467-947A-8
20	314	16.9	373	3	US-08-513-974B-373
21	308	16.6	325	5	US-08-118-270-51
22	308	16.6	325	5	PCT-US93-08528-51
23	307	16.6	391	1	US-07-816-283-4
24	307	16.6	391	1	US-08-417-103-4
25	307	16.6	395	1	US-08-097-958-5
26	307	16.6	395	1	US-08-476-000-5
27	307	16.6	395	1	US-08-472-840-5

28	307	16.6	395	2	US-08-476-976-5	Sequence 5, Appl1
29	307	16.6	395	3	US-08-474-410-5	Sequence 5, Appl1
30	306	16.5	398	1	US-08-097-938-6	Sequence 6, Appl1
31	306	16.5	398	1	US-08-476-000-6	Sequence 6, Appl1
32	306	16.5	398	1	US-08-472-840-6	Sequence 6, Appl1
33	306	16.5	398	2	US-08-476-976-6	Sequence 6, Appl1
34	306	16.5	398	3	US-08-474-410-6	Sequence 6, Appl1
35	306	16.5	398	4	US-08-486-673B-6	Sequence 6, Appl1
36	305.5	16.5	369	4	US-08-120-601B-9	Sequence 9, Appl1
37	305.5	16.5	391	1	US-07-816-283-2	Sequence 2, Appl1
38	305.5	16.5	391	1	US-08-417-103-2	Sequence 2, Appl1
39	305.5	16.5	391	1	US-08-417-103-14	Sequence 14, Appl1
40	305	16.5	337	4	US-09-044-404A-2	Sequence 2, Appl1
41	303.5	16.4	391	4	US-08-120-601B-8	Sequence 8, Appl1
42	302.5	16.3	369	1	US-07-816-283-6	Sequence 6, Appl1
43	302.5	16.3	369	1	US-08-417-103-6	Sequence 6, Appl1
44	302.5	16.3	369	1	US-08-417-103-16	Sequence 16, Appl1
45	302	16.3	364	4	US-08-148-708-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5953308
GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: MOONEY, JEFFREY
; APPLICANT: BERGSMAN, DERK
; APPLICANT: HALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEQD054 THAT ENCODES A HUMAN 7-TRANS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955, 713
; FILING DATE: 23-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050, 124
; FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 423 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-955-713-2
Query Match 28.5%; Score 529; DB 2; Length 423;
Best Local Similarity 39.2%; Pred. No. 3.9e-38;
Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

[illegible]

RESULT 5
 US-08-513-974B-374
 ; Sequence 374, Application US/08513974B
 ; Patent No. 6114139

APPLICANT: Hinuma, Shuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ohtaki, Tetsuya
 APPLICANT: Fukushima, Shoji
 APPLICANT: Ohai, Kazuhiko
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34, 235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-374

```

```

Query Match          20.0% Score 371; DB 3; Length 362;
Best Local Similarity 29.1% Pred No. 1.4e-24;
Matches 95; Conservative 60; Mismatches 128; Indels 44; Gaps 7;

```

```

QY 18 MPPLIIVAFVLGALNGVALGCGCFHMKTKPSTVYLEFNLAIVADFLIMICLPFRDYLLR 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 43 LPVYILVIFLIGFNGSVALIMFEVFMHMPGSGISYVFNLADELVLPLPILFYFN 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 RRHAFDIPCRVGLFTLANRAGSIVFLVVAADRFKVVHPHNAVNTISTVAAAGIYC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 103 KIDWIFGDWCKIQRFIFVNLXGSLFLTCISVHRGTGVHPLSLGRLKKNAYISV 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 TLMALVILGTYYLLLEHNL-----CVQETA-----VSCSEFIMESANGMHD 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 163 LVMALVAVAIAPILFYSIGVGRNNTITCYDTADEYLRSIFYVSMCTVFN----- 214
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 IMFQLEFFMPGLILFCSEFKIWSLRRQOLARQARKKATRFINVAIVFTCYLP--- 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 215 -----FCIPFTIILGCGYLIYKALYK-DLDSPLRRKSTVILVITLFAVSYLEPHV 267
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 ----SVSATLYFLMTVPSSACDPVHGALHTLSFTYVNSMDPLVYFSSSFKFYFNK 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 268 MRTLNRALDF-QTPOMCAFNDKVATYQVTRGLASLNSCVDPLIYLAGDTFRRLSR 326
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 LKICSLKPKQGHSKTORPEEMPISNL 318
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 327 ATRKSSRSEP--NVQSKSEMTNL 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 6
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08-559-524A-4

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

```

```

Query Match          19.6% Score 362.5; DB 2; Length 373;
Best Local Similarity 27.5% Pred No. 7.9e-24;
Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;

```

```

QY 18 MPPLIIVAFVLGALNGVALGCGCFHMKTKPSTVYLEFNLAIVADFLIMICLPFRDYLLR 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 54 LPVYILVIFLIGFNGSVALIMFEVFMHMPGSGISYVFNLADELVLPLPILFYFN 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 78 RRHAFDIPCRVGLFTLANRAGSIVFLVVAADRFKVVHPHNAVNTISTVAAAGIYC 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 KIDWIFGDWCKIQRFIFVNLXGSLFLTCISVHRGTGVHPLSLGRLKKNAYISV 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 138 TLMALVILGTYYLLLEHNL-----AVSC-----ESFIMESANGMHDIFQLEFFM 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 174 LVMALVAVAIAPILFYSIGVGRNNTITCYDTADEYLRSIFYVSMCTVFN----- 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 PLGILFCSEFKIWSLRRQOLARQARKKATRFINVAIVFTCYLP-----SVSAR 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 229 PLVILIGCGYLIYKALYK-DLDSPLRRKSTVILVITLFAVSYLEPHV 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 LYLMTVPSSACDPVHGALHTLSFTYVNSMDPLVYFSSSFKFYFNK 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 288 LDF-QTPOMCAFNDKVATYQVTRGLASLNSCVDPLIYLAGDTFRRLSR----- 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 QPCHSKTORPEEMPISNLGRRSCISVANSFQSD 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 338 --ATRKSSRSEPANLQSKSEMTNLINISFKQNGD 370
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 7
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707

```



```

1 FILING DATE: 15-NOV-1996
2 CLASSIFICATION: 536
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Adler, Reid G.
5 REGISTRATION NUMBER: 30,988
6 REFERENCE/DOCKET NUMBER: 04481-5010-01-US
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 202-467-7000
9 TELEFAX: 202-467-7176
10 INFORMATION FOR SEQ ID NO: 4:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 373 amino acids
13 TYPE: amino acid
14 STRANDEDNESS:
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17 US-08-749-707-4

```

Query Match	19.6%;	Score 362.5;	DB 3;	Length 373;
Best Local Similarity	27.5%;	Pred. No. 7.9e-24;		
Matches 92;	Conservative 68;	Mismatches 140;	Indels 35;	Gaps 7;

```

OY 18 MPELLIYFVGLANGVALGCEFHMMTKWSTYVLEFLWADFLMLCEPFRDYLR 77
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 54 LPAYVILYFIIFLGNLSVAIMFMFVHMKPMWSISYMFMLADLLYLTELALFYFN 113
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 78 RHHMAFGDIPCEVGLFPTLAMNAGSIVELYVADRYEKVPHHNAVNTISRYAAGIVC 137
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 KTDWTFGDMCKLOFIEFHVNLGYSILEFPTCISAHRYSGVVYPLKSLGKMKKNAYISV 173
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 138 TLMVAIYIGTVYLLLENHLVQET- AVSC-----ESFIMESANGHMDIMOLEPMA 187
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 LVMILVVYGISPILEYSGGIRKNNITITICDTSDEILSRFYLYSM-----CTYAMPCV 228
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 188 PLGITLFCFSFKVMSLRRRQOLARQARMKKATRFIMVYAIVITTCYLP-----SVSKR 240
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 229 PLVLLIGCGGLLRALRYK-DLDNSPLRKRSLYLVIAIVTYAVASYIPHYAKTMYMLRAR 287
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 241 LYFLMTVSSACDPVHGHLHTLTSFTYVNSMLDPLVYFYFSSPFPKFNKLCISLKP 300
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 288 LDF-QTPEMCAVNDRYATYVTRGLASLNSCVDPILEYLADDTFRRRLSR----- 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 301 QPHGSKTQREPMPISNLGRSCISVANSFOQSD 335
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 338 --ATRKASRSEANLQSKSEDMTMLNLSFEKONGD 370
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

? RESULT 8
? US-08-781-250-2
? Sequence 2, Application US/08781250
? Patent No. 6010877
? GENERAL INFORMATION:
? APPLICANT: Sathe, Ganesh
? APPLICANT: Van Horn, Stephanie
? APPLICANT: Bergsma, Derk
? APPLICANT: Mao, Joyce Yue
? TITLE OF INVENTION: CDNA CLONE HB8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Smithsonian Beecham
? STREET: 709 Swedeland Road
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION NUMBER: US/08/781,250
? FILING DATE: 10-JAN-1997

```

```

1 CLASSIFICATION: 514
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER:
4 FILING DATE:
5 ATTORNEY/AGENT INFORMATION:
6 NAME: William T. Han,
7 REGISTRATION NUMBER: 34,344
8 REFERENCE/DOCKET NUMBER: AIG50043
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 610-270-5219
11 TELEFAX: 610-270-4060
12 TELEX:
13 INFORMATION FOR SEQ ID NO: 2:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 370 amino acids
16 TYPE: amino acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: protein
20
21 US-08-781-250-2

```

Query Match	18.7%;	Score 346.5;	DB 3;	Length 370;
Best Local Similarity	31.2%;	Pred. No. 1.9e-22;		
Matches 95;	Conservative 52;	Mismatches 128;	Indels 29;	Gaps 11;

OY	24	VAFVGLANGNGVALCGFCFCHMKTKWPSYUWLVADFLMATICPFRTDYILRRHNAF	83
	1	: : : : : : : : : : :	
Db	48	VVFILIGLITNSVSLFVFCRMRKMRETAFLITNLAVSDLEFUCITLPEK - FVNPNHMF	106
OY	84	GDIPCRVGLITLANNBAGIVFLVYVADRKYVKNPHNAVTISIRVAGIVCT - LMAI	142
	1	: : : : : : : : : :	
Db	107	GMTICKISGTAPLITMYSGMLFLTCISVDFALAIYPPRS - RTIKRNSAIVCAGWLL	165
OY	143	VILGTIVYLLLEHLHCVOETAVASC - ESFIMESANGMHIDFOLE ----- FMPALGILF	194
	1	: : : : : : : : : :	
Db	166	VLSGGISASLSEFTTNVNNMTTCPEGE - -SKRVKTYLSKITIFIEVVGFIILPLANS	222
OY	195	CSFKIYVMSIRRQOOLAR -OARMKKATRTIMVVAIVFITCYLSSVSKRLYFLMTVPSSAC -	252
	1	: : : : : : : : : :	
Db	223	CSSVYLRTLRKATLISQIDTNRKKYLMKMTYMAAFVVCFFVPRS - VLEVLAVNSQAI	280
OY	253	-----DPSVHGAHLITLSEFTYNNMSMLDPLVYXYFSSSPFK - FYNKLKILSLKPKOGHAK	306
	1	: : : : : : : : : :	
Db	281	TNCFLERFKAIMYPIILCIATLINCSDPLIYFETLESFCKSFYIANKI ----- RMESLEPK	335
OY	307	TQRP 310	
	1	: : : : : : : : : :	
Db	336	TEPR 339	

```

1  RESULT 9
2  US-08-153-848-44
3  : Sequence 44, Application US/08153848
4  : Patent No. 5759804
5  :
6  : GENERAL INFORMATION:
7  :
8  : APPLICANT: Godiska, Ronald
9  : APPLICANT: Gray, Patrick W.
10 : APPLICANT: Schweikart, Vicki L.
11 : TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
12 :
13 : NUMBER OF SEQUENCES: 64
14 :
15 : CORRESPONDENCE ADDRESS:
16 :
17 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
18 : ADDRESSEE: Ricknell
19 : STREET: 6300 Sears Tower, 233 South Wacker Drive
20 :
21 : CITY: Chicago
22 :
23 : STATE: Illinois
24 :
25 : COUNTRY: USA
26 :
27 : ZIP: 60606
28 :
29 : COMPUTER READABLE FORM:
30 :
31 : MEDIUM TYPE: Floppy disk
32 :
33 : COMPUTER: IBM PC compatible
34 :
35 : OPERATING SYSTEM: PC-DOS/MS-DOS
36 :
37 : SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-44

```

```

Query Match      18.1%; Score 336; DB 1; Length 339;
Best Local Similarity 30.5%; Pred. No. 1.4e-21;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

```

```

QY 7 CRLEDITISQVMPPLLIYAVLGAALGNGVALGCFCEHMKTKWSPYVYLFNLAVADFLMI 66
DB 23 CGQETPLENNLAFSPYLLDFILALVGNLTALMLFIDHKSQTPANVFLMHLAVADSLCVL 82
QY 67 CLPRTDYILRRHWAAGDIPCRVGLFTLANRAGSIVELTVVADRYEKVHPHHAVNT 126
DB 83 VLPTRLVYHFGSNHWPFGELACRLTGFLFLYLMYASIVELTCSADRFALVHP--VKS 139
QY 127 ISTR--VAAGIVCT-LMALVILGTVYLLLENHLCVQETAVSCSEPTMESANCMHDIMQQL 183
DB 140 LKLRPLVLAHLACAFLLMVAAMAPLVSQTVQTNHTVVCLOLYRKASHHALLSLAV 199
QY 184 EFMPLGLIILFCSEKIVWSLRRQOLARQARK-KATREIMVAIVETTCYLP-SVSARL 241
DB 200 AFTEPFTVTVCYLLIIRSL--RQGLRVKRLKTKAVRMIAIVLALFVLCVPYHVNRSV 257
QY 242 YFL--WTVPSSACDPVHGAL--HTLSFTYMSMDPLVYFFSSSPFKFNKLKICSUK 298
DB 258 YVLHTRSHGASCATQRIILANRITSLTSLNGALDPIWTFVAEKFRHALCNL-LCGKR 316
QY 299 PKPGHSKTQPREMPIS 316
DB 317 LKGPPEPFEGKTNESSLS 334

```

```

RESULT 10
US-08-812-871-3
Sequence 3, Application US/08812871
Patent No. 5955303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong, Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

```

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
US-08-812-871-3

```

```

Query Match      18.1%; Score 336; DB 2; Length 339;
Best Local Similarity 30.5%; Pred. No. 1.4e-21;
Matches 97; Conservative 54; Mismatches 153; Indels 14; Gaps 9;

```

```

QY 7 CRLEDITISQVMPPLLIYAVLGAALGNGVALGCFCEHMKTKWSPYVYLFNLAVADFLMI 66
DB 23 CGQETPLENNLAFSPYLLDFILALVGNLTALMLFIDHKSQTPANVFLMHLAVADSLCVL 82
QY 67 CLPRTDYILRRHWAAGDIPCRVGLFTLANRAGSIVELTVVADRYEKVHPHHAVNT 126
DB 83 VLPTRLVYHFGSNHWPFGELACRLTGFLFLYLMYASIVELTCSADRFALVHP--VKS 139
QY 127 ISTR--VAAGIVCT-LMALVILGTVYLLLENHLCVQETAVSCSEPTMESANCMHDIMQQL 183
DB 140 LKLRPLVLAHLACAFLLMVAAMAPLVSQTVQTNHTVVCLOLYRKASHHALLSLAV 199
QY 184 EFMPLGLIILFCSEKIVWSLRRQOLARQARK-KATREIMVAIVETTCYLP-SVSARL 241
DB 200 AFTEPFTVTVCYLLIIRSL--RQGLRVKRLKTKAVRMIAIVLALFVLCVPYHVNRSV 257
QY 242 YFL--WTVPSSACDPVHGAL--HTLSFTYMSMDPLVYFFSSSPFKFNKLKICSUK 298
DB 258 YVLHTRSHGASCATQRIILANRITSLTSLNGALDPIWTFVAEKFRHALCNL-LCGKR 316
QY 299 PKPGHSKTQPREMPIS 316
DB 317 LKGPPEPFEGKTNESSLS 334

```

```

RESULT 11
US-09-299-843A-44
Sequence 44, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA

```

RESULT 12
 US-09-088-337B-44
 : Sequence 44, Application US/09088337B
 : Patent No. 6348574
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Godiska, Ronald
 : Gray, Patrick W.
 : Schwellbart, Vicki L.
 :
 : TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptorlors
 :

```

RESULT 13
PCT-US93-11153-44
; Sequence 44, Application PC/TUS9311153
; GENERAL INFORMATION:

```

```

1  APPLICANT:  Godiska, Ronald
2  APPLICANT:  Gray, Patrick W.
3  APPLICANT:  Schmelkart, Vicki L.
4  TITLE OF INVENTION:  Novel Seven Transmembrane Receptors
5  NUMBER OF SEQUENCES:  64
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
8  ADDRESSEE:  Bicknell, 233 South Wacker Drive
9  STREET:  6300 Sears tower, 233 South Wacker Drive
10 CITY:  Chicago
11 STATE:  Illinois
12 COUNTRY:  USA
13 ZIP:  60606
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE:  Floppy disk
17 COMPUTER:  IBM PC compatible
18 OPERATING SYSTEM:  PC-DOS/MS-DOS
19 SOFTWARE:  Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER:  PCT/US93/11153
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  US 07/977,452
26 FILING DATE:  17-NOV-1992
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Noland, Greta E.
29 REGISTRATION NUMBER:  35,302
30 REFERENCE/DOCKET NUMBER:  31794
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  (312) 474-6300
33 TELEFAX:  (312) 474-0448
34 TELEX:  25-3856
35 INFORMATION FOR SEQ ID NO:  44:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH:  339 amino acids
38 TYPE:  amino acid
39 TOPOLOGY:  linear
40 MOLECULE TYPE:  protein
41 PCT-US93-11153-44

```


GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 19:38:54 ; Search time 34 Seconds
(without alignments)
597.600 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853

Sequence: 1 MYNSCCRIEGDITISQVMP.....ANSFQSQSDGQMDPIHEWMH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1853	100.0	346	10	US-09-862-274-2
2	1853	100.0	346	10	US-09-942-374-2
3	1849	99.8	346	9	US-10-094-417-8
4	1739	93.8	342	9	US-10-092-135-2
5	880.5	47.5	387	9	US-10-092-135-8
6	880.5	47.5	387	10	US-09-944-807-21
7	529	28.5	423	10	US-09-826-508-40
8	448.5	24.1	319	9	US-10-092-135-9
9	446.5	24.1	319	9	US-10-109-549-2
10	366.5	19.8	330	10	US-09-826-791-2
11	366.5	19.8	346	9	US-09-828-478-2
12	366.5	19.8	346	10	US-09-826-791-6
13	366.5	19.8	346	10	US-09-866-230-7
14	366.5	19.8	346	10	US-09-866-230-9
15	364	19.6	362	9	US-10-092-135-3
16	364	19.6	362	9	US-10-092-135-4
17	362.5	19.6	373	9	US-10-092-135-5
18	358.5	19.3	373	9	US-10-092-135-7
19	354	19.1	373	9	US-10-092-135-6

20	343	18.5	299	9	US-10-270-144-4	Sequence 4, Appli
21	336	18.1	339	9	US-09-828-478-4	Sequence 4, Appli
22	336	18.1	339	10	US-09-848-689-12	Sequence 12, Appli
23	336	18.1	339	10	US-09-788-133-2	Sequence 2, Appli
24	336	18.1	367	9	US-09-828-478-6	Sequence 6, Appli
25	328.5	17.7	302	9	US-10-024-494-30	Sequence 30, Appli
26	327	17.6	309	10	US-09-768-877-20	Sequence 20, Appli
27	325	17.5	344	9	US-10-024-494-8	Sequence 8, Appli
28	320	17.3	341	9	US-10-270-587-3	Sequence 3, Appli
29	318	17.2	253	9	US-10-116-252-10	Sequence 10, Appli
30	309.5	16.7	363	9	US-09-992-331-14	Sequence 14, Appli
31	305.5	16.5	391	9	US-09-990-940-20	Sequence 20, Appli
32	305	16.5	337	9	US-09-828-478-5	Sequence 5, Appli
33	305	16.5	337	10	US-09-866-230-8	Sequence 8, Appli
34	305	16.5	372	10	US-10-167-192-5	Sequence 5, Appli
35	305	16.5	372	10	US-09-768-894A-2	Sequence 2, Appli
36	302	16.3	337	9	US-10-167-192-3	Sequence 3, Appli
37	302	16.3	391	12	US-09-966-871-82	Sequence 82, Appli
38	302	16.3	391	12	US-10-039-645-82	Sequence 82, Appli
39	300.5	16.2	369	10	US-09-823-114-9	Sequence 9, Appli
40	300	16.2	428	9	US-09-992-331-15	Sequence 15, Appli
41	298.5	16.1	418	9	US-09-992-331-17	Sequence 17, Appli
42	298	16.1	428	9	US-09-992-331-16	Sequence 16, Appli
43	294	15.9	372	9	US-10-112-599A-4	Sequence 4, Appli
44	293	15.8	362	9	US-09-992-331-13	Sequence 13, Appli
45	292.5	15.8	365	9	US-10-109-533A-2	Sequence 2, Appli

ALIGNMENTS

1

RESULT 1
US-09-862-274-2
Sequence 2, Application US/09862274
Patent No. US20020052022A1
GENERAL INFORMATION:
APPLICANT: ELSHOURBAGY, NABIL
APPLICANT: GATTU, MAHANANDESHWAR
APPLICANT: SHABON, USMAN
APPLICANT: IGAR, DIANE MICHELE
TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE
FILE REFERENCE: GP-70703-1
CURRENT APPLICATION NUMBER: US/09/862,274
CURRENT FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 09/580,675
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: GB 0026839.1
PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-862-274-2

Query Match 100.0% Score 1853; DB 10; Length 346;
Best Local Similarity 100.0% Pred. No. 1,6e-169;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNSCCRIEGDITISQVMPPLIYFVIGALGNGVALGFCFHHKTKPSTVYLFNLAVA 60
DB 1 MYNSCCRIEGDITISQVMPPLIYFVIGALGNGVALGFCFHHKTKPSTVYLFNLAVA 60
QY 61 DELMATICPEFRDYLLRRRHHAFGDI PCRVGLFTLANRAGSIYELTVVADRYFKYVHP 120
DB 61 DELMATICPEFRDYLLRRRHHAFGDI PCRVGLFTLANRAGSIYELTVVADRYFKYVHP 120
QY 121 HHAVNTISTRVAAAGIVCTLMALVILGTYLLLENHLCKQETFAVCESTFMSANGMDIM 180
DB 121 HHAVNTISTRVAAAGIVCTLMALVILGTYLLLENHLCKQETFAVCESTFMSANGMDIM 180

QY 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346

RESULT 2
 US-09-942-374-2
 ; Sequence 2, Application US/09942374
 ; Patent No. US20020137063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Gimeno, Ruth
 ; APPLICANT: White, David
 ; TITLE OF INVENTION: 57242, a Human G-Protein Coupled
 ; TITLE OF INVENTION: Receptor Family Member and Uses therefor
 ; FILE REFERENCE: MP12000-368P1R
 ; CURRENT APPLICATION NUMBER: US/09/942,374
 ; CURRENT FILING DATE: 2001-08-29
 ; PRIOR APPLICATION NUMBER: US 60/228,409
 ; PRIOR FILING DATE: 2000-08-29
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-942-374-2

Query Match 100.0%; Score 1853; DB 10; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1,6e-169;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYNSGCCRIEGDTSQVMPPLLIYAFVLGALGNGVALGCFCHMKTKPSTYVLENLAVA 60
 DB 1 MYNSGCCRIEGDTSQVMPPLLIYAFVLGALGNGVALGCFCHMKTKPSTYVLENLAVA 60
 QY 61 DFLMTCLEPFRDYYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 DB 61 DFLMTCLEPFRDYYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 QY 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346

RESULT 3
 US-10-094-417-8
 ; Sequence 8, Application US/10094417
 ; Publication No. US20030045685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Zhao, Jiaqiang
 ; APPLICANT: Chen, Jin-Long

APPLICANT: Cutler, Gene
 APPLICANT: Tularik Inc.
 TITLE OF INVENTION: No. US20030045685A1el Receptors
 FILE REFERENCE: 018781-008110US
 CURRENT APPLICATION NUMBER: US/10/094,417
 CURRENT FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: US 09/802,803
 PRIOR FILING DATE: 2001-03-09
 PRIOR APPLICATION NUMBER: US 60/276,649
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR183
 US-10-094-417-8

Query Match 99.8%; Score 1849; DB 9; Length 346;
 Best Local Similarity 99.7%; Pred. No. 3,9e-169;
 Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MYNSGCCRIEGDTSQVMPPLLIYAFVLGALGNGVALGCFCHMKTKPSTYVLENLAVA 60
 DB 1 MYNSGCCRIEGDTSQVMPPLLIYAFVLGALGNGVALGCFCHMKTKPSTYVLENLAVA 60
 QY 61 DFLMTCLEPFRDYYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 DB 61 DFLMTCLEPFRDYYLRRRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 QY 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 DB 121 HHAVENTISTRVAAGIVCTLMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGMHDIM 180
 QY 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 DB 181 FOLEFMPGLIIFCSFKIYWSLRROQLARQARKKATRFIMVAIVITCYLPVSAR 240
 QY 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 DB 241 LYFLMTVPSSACDPVSHGALHITLSTFTYNSMLDPLVYFSSPSPKFKYKLIKISLKP 300
 QY 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346
 DB 301 QPGHSTQRPPEMPISNLGRSCISVANSFOSODGOMDPHIVEWH 346

RESULT 4
 US-10-092-135-2
 ; Sequence 2, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 342
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-092-135-2

Query Match 93.8%; Score 1739; DB 9; Length 342;

Db 256 WLHTSGTQNCVEYKSVDLAFITLESFTYMSMDPVVYFYSSPSPEPFSTLINRCLQR 315

Db 316 KMTGEPDNNRSTSVETGDPNKT - RGAPEALMANGGEPNSP 355

RESULT 6
US-09-944-807-21

Patent No. US20020119494A1

; TITLE OF INVENTION: Method for identifying substances which positively
 ; TITLE OF INVENTION: influence inflammatory conditions of chronic

```

; FILE REFERENCE: 082_00n
; CURRENT APPLICATION NUMBER: US/09/944,807

```

```

; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01

```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21

```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; 15 00 014 007

```

Query Match	Score	DB	Length
47.5%	880.5	10	387

Matches	1/8; Conservative	49; Mismatches	107; Indels	7; Gaps
5	5000	5000	5000	5000

Dp 17 NCCVERDFAIAKVLPPVLGLFEIFIGLLGNGLALWIFCFHLKSWKSSRIFFLENLAVADELL 76

```

05 MCLPERIDYLLERRHWAFFGIDIPRVGLFTLAMNRGSIVFLTVAADRYFKVHPHNAV 124
06 :::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
07 TICTPEVMDYVERSDMNEGDTPORIVTEMLAMNPGOSTTEUYVAVDVEDPVYUQUTAT 126
08 :::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

```

QY 125 N1STRVAGIYCTLMALVILGIVYLLLENHLCVOETAVSCSEFINESANGWHDIMEOLE 184

185 FEMPLGIIIFCEFKIWSLRROOLAROBKMKATREIMVAIVETTCYIPSVSARIYEL. 244
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200

Db 197 FLPLGLFCSARTISLRQR-QMDRHAQIKRATFIMVAIVEVICFLPSVVVRIRIF 255

256 WLHTSGTQNCVYRSVDLAEFTITLSTFYMNSMDLPVYVFSSPSNFEFTLLINCRQI 315

```
QY      300 KQPGHSTQRPPEMPISNLGRSCISVANSFQSDGQWDP 340
      | | | | | : : : : : : : : | |
      | | | | | : : : : : : : : | |
```

US-09-826-508-40
: Sequence 40, Application US/09826508

```

; GENERAL INFORMATION:
;
; APPLICANT: Nabil Elshourbagy

```

1. TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides

CURRENT APPLICATION NUMBER: US/09/826,508
 CURRENT FILING DATE: 2001-04-05
 NUMBER OF SEQ. ID NOS.: 10

```

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40

```



```

; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-2

```

```

Query Match          19.8%; Score 366.5; DB 10; Length 330;
Best Local Similarity 29.9%; Pred. No. 2,8e-27;
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

```

```

QY 3 NSGCRIGEDTISQVMPPLIIVAFVGLGNGVALGCGFCHMKTKPST---VYLENLAV 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 11 NSRNCIE-NKREFPIYVLIIFGNGSIYF---LQPYKSTSVNFMNLAI 66
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 ADFLMICLPFRDYLRHMAFGDIPCRVGLFTLMMNRAGSIVFLTVAADRYKVVH 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 SDLFISTLPFRADYLRGSMWIFGDLACRIMSYSLVNMYSITFLTVSVRFAMVH 126
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 PHNAVNTISTRVAGIVCTLMALVILGTYLLLENHLCVOETAVSC---ESFIMESANGW 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 127 PFRLLHVTISR-SAMILGCIWILMASSIMLDGSEONGSVTSCLELNLYKIAKLOTM 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 HDIMFOLEFEMPGLGILFCSEFKIWSLRRRO--QLARQARKKATRFIMVAIVETCYL 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 186 NYIALVGGCLPFTSTICLLIRVLKVEPESGLRVSHRKALTTITTLIFLFCFL 245
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMLDPLVYESSPSPKPYNKIKI 294
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 246 PYHTLRVHLTWKVGCKDRLHKALVITLALAAANACFNPLIYFAGENFK---DRLK- 301
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 CSLKPKPGHSTQ 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 302 SALRKGHPOKAKTK 315
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 11

```

US-09-828-478-2
; Sequence 2, Application US/09828478
; Patent No. US2002015528A1
; GENERAL INFORMATION:
; APPLICANT: Xlao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 049/4.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-478-2

```

```

Query Match          19.8%; Score 366.5; DB 9; Length 346;
Best Local Similarity 29.9%; Pred. No. 3e-27;
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

```

```

QY 3 NSGCRIGEDTISQVMPPLIIVAFVGLGNGVALGCGFCHMKTKPST---VYLENLAV 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 27 NSRNCIE-NKREFPIYVLIIFGNGSIYF---LQPYKSTSVNFMNLAI 82
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 ADFLMICLPFRDYLRHMAFGDIPCRVGLFTLMMNRAGSIVFLTVAADRYKVVH 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 SDLFISTLPFRADYLRGSMWIFGDLACRIMSYSLVNMYSITFLTVSVRFAMVH 142
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 PHNAVNTISTRVAGIVCTLMALVILGTYLLLENHLCVOETAVSC---ESFIMESANGW 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

DB 143 PFRLLHVTISR-SAMILGCIWILMASSIMLDGSEONGSVTSCLELNLYKIAKLOTM 201
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 HDIMFOLEFEMPGLGILFCSEFKIWSLRRRO--QLARQARKKATRFIMVAIVETCYL 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 NYIALVGGCLPFTSTICLLIRVLKVEPESGLRVSHRKALTTITTLIFLFCFL 261
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMLDPLVYESSPSPKPYNKIKI 294
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 262 PYHTLRVHLTWKVGCKDRLHKALVITLALAAANACFNPLIYFAGENFK---DRLK- 317
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 CSLKPKPGHSTQ 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 318 SALRKGHPOKAKTK 331
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 12

```

US-09-826-791-6
; Sequence 6, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: No. US20010039037A1 polypeptide
; FILE REFERENCE: PCI0914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 0008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-6

```

```

Query Match          19.8%; Score 366.5; DB 10; Length 346;
Best Local Similarity 29.9%; Pred. No. 3e-27;
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

```

```

QY 3 NSGCRIGEDTISQVMPPLIIVAFVGLGNGVALGCGFCHMKTKPST---VYLENLAV 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 27 NSRNCIE-NKREFPIYVLIIFGNGSIYF---LQPYKSTSVNFMNLAI 82
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 ADFLMICLPFRDYLRHMAFGDIPCRVGLFTLMMNRAGSIVFLTVAADRYKVVH 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 83 SDLFISTLPFRADYLRGSMWIFGDLACRIMSYSLVNMYSITFLTVSVRFAMVH 142
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 PHNAVNTISTRVAGIVCTLMALVILGTYLLLENHLCVOETAVSC---ESFIMESANGW 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 143 PFRLLHVTISR-SAMILGCIWILMASSIMLDGSEONGSVTSCLELNLYKIAKLOTM 201
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 HDIMFOLEFEMPGLGILFCSEFKIWSLRRRO--QLARQARKKATRFIMVAIVETCYL 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 NYIALVGGCLPFTSTICLLIRVLKVEPESGLRVSHRKALTTITTLIFLFCFL 261
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMLDPLVYESSPSPKPYNKIKI 294
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 262 PYHTLRVHLTWKVGCKDRLHKALVITLALAAANACFNPLIYFAGENFK---DRLK- 317
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 295 CSLKPKPGHSTQ 308
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 318 SALRKGHPOKAKTK 331
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 13

```

US-09-866-230-7
; Sequence 7, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.

```

TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-866-230-7

Query Match 19.8%; Score 366.5; DB 10; Length 346;
Best Local Similarity 29.9%; Pred. No. 3e-27;
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

QY 3 NSGCCRIEADTISQVMPPLIIVAFVLAGNGVALCGFCFHMKTWKPST---VYLEFNLA 59
DB 27 NSRNCTIE-NFKREFFPIVYLIIFFWGLNGLSIYF---LQPYKSTSVNFMNLAI 82
QY 60 ADELMTLCPTRTDYLLRRRMAGSDIPCRVGLFTLAMNRAGSIVFLVAADREKVVH 119
DB 83 SDLEFISTLPFRADYLLRGSWMIFGDLACRIMSLSLVNMTSIVFVLVSREFLAMVH 142
QY 120 PHNAVNTSTRVAGIVCTLMALVIGVYLLLENHLCVQETASC---ESFIMESANGW 176
DB 143 PFRLLHVTISR-SAMILCGIITWILMASSIMLDSGEONSVSCELNITKAKIOTM 201
QY 177 HDIMFQLEFFMPGLIILFCSEFKIWSLRRO--QLARQARKKATREFIMVAIVITCYL 234
DB 202 NYIALVVGCLLPFTLSTICYLIIIRVLKVEPESGLRSHRKALTTIITLIIFLCEL 261
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMDLPVYFSSSPKFTYNNLKI 294
DB 262 PYHTLRVTHTWVGLCKDRHLKALVITTLAANAACENPLLYFAGENFR---DRLK- 317
QY 295 CSIKRKOPGHSKTQ 308
DB 318 SALRKGHPOKAKTK 331

RESULT 14
US-09-866-230-9
Sequence 9, Application US/09866230
GENERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/207,725
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-866-230-9

Query Match 19.8%; Score 366.5; DB 10; Length 346;
Best Local Similarity 29.9%; Pred. No. 3e-27;
Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

QY 3 NSGCCRIEADTISQVMPPLIIVAFVLAGNGVALCGFCFHMKTWKPST---VYLEFNLA 59
DB 27 NSRNCTIE-NFKREFFPIVYLIIFFWGLNGLSIYF---LQPYKSTSVNFMNLAI 82
QY 60 ADELMTLCPTRTDYLLRRRMAGSDIPCRVGLFTLAMNRAGSIVFLVAADREKVVH 119
DB 83 SDLEFISTLPFRADYLLRGSWMIFGDLACRIMSLSLVNMTSIVFVLVSREFLAMVH 142
QY 120 PHNAVNTSTRVAGIVCTLMALVIGVYLLLENHLCVQETASC---ESFIMESANGW 176
DB 143 PFRLLHVTISR-SAMILCGIITWILMASSIMLDSGEONSVSCELNITKAKIOTM 201
QY 177 HDIMFQLEFFMPGLIILFCSEFKIWSLRRO--QLARQARKKATREFIMVAIVITCYL 234
DB 202 NYIALVVGCLLPFTLSTICYLIIIRVLKVEPESGLRSHRKALTTIITLIIFLCEL 261
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMDLPVYFSSSPKFTYNNLKI 294
DB 262 PYHTLRVTHTWVGLCKDRHLKALVITTLAANAACENPLLYFAGENFR---DRLK- 317
QY 295 CSIKRKOPGHSKTQ 308
DB 318 SALRKGHPOKAKTK 331

DB 83 SDLEFISTLPFRADYLLRGSWMIFGDLACRIMSLSLVNMTSIVFVLVSREFLAMVH 142
QY 120 PHNAVNTSTRVAGIVCTLMALVIGVYLLLENHLCVQETASC---ESFIMESANGW 176
DB 143 PFRLLHVTISR-SAMILCGIITWILMASSIMLDSGEONSVSCELNITKAKIOTM 201
QY 177 HDIMFQLEFFMPGLIILFCSEFKIWSLRRO--QLARQARKKATREFIMVAIVITCYL 234
DB 202 NYIALVVGCLLPFTLSTICYLIIIRVLKVEPESGLRSHRKALTTIITLIIFLCEL 261
QY 235 PSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMDLPVYFSSSPKFTYNNLKI 294
DB 262 PYHTLRVTHTWVGLCKDRHLKALVITTLAANAACENPLLYFAGENFR---DRLK- 317
QY 295 CSIKRKOPGHSKTQ 308
DB 318 SALRKGHPOKAKTK 331

RESULT 15
US-10-092-135-3
Sequence 3, Application US/10092135
Publication No. US20030054374A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPT
FILE REFERENCE: D0134.NP
CURRENT APPLICATION NUMBER: US/10/092,135
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US 60/273,808
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/278,983
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 362
TYPE: PRT
ORGANISM: GALLUS GALLUS
US-10-092-135-3

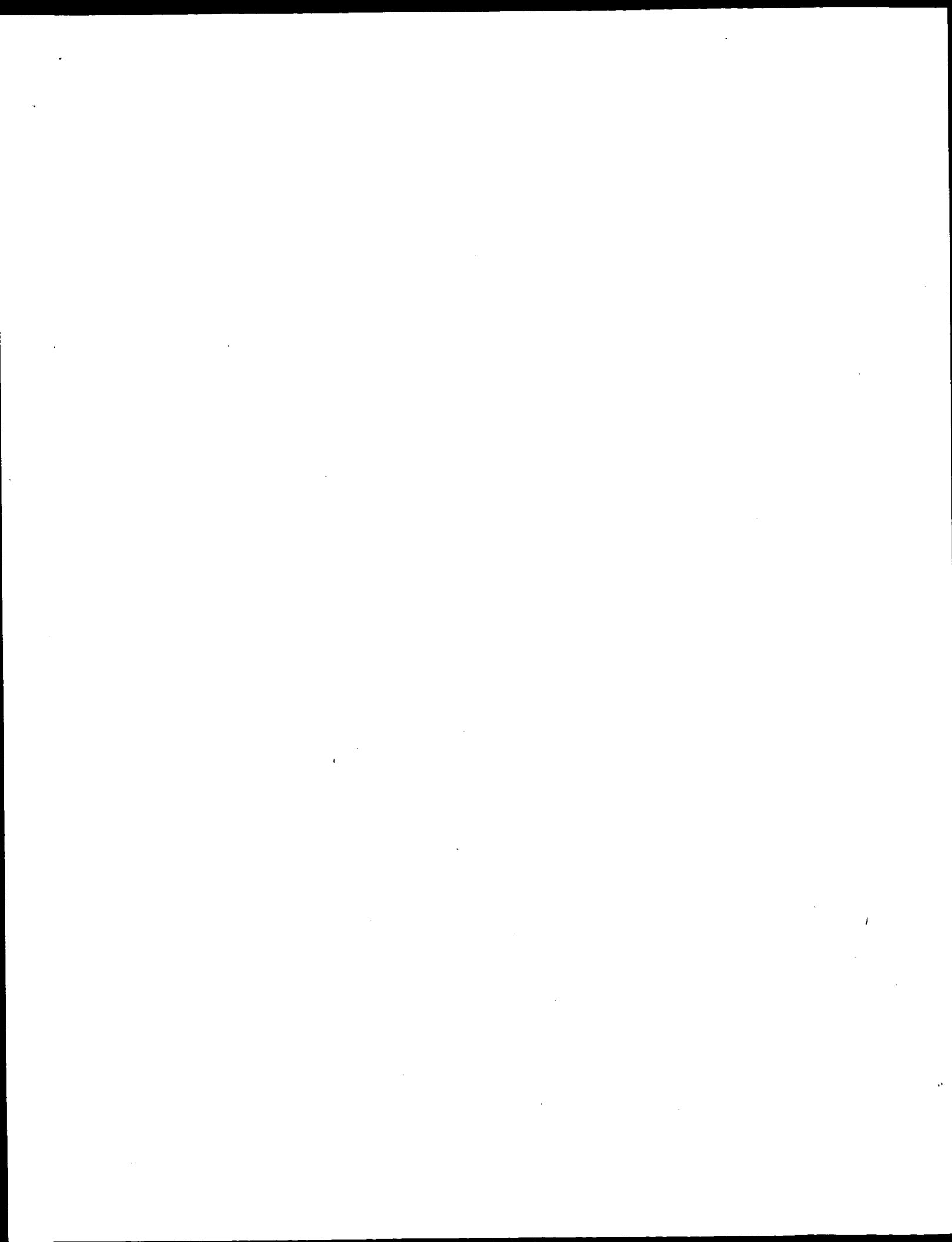
Query Match 19.6%; Score 364; DB 9; Length 362;
Best Local Similarity 29.1%; Pred. No. 5.4e-27;
Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPPLIIVAFVLAGNGVALCGFCFHMKTWKPSTVYLFNLAADFLMCLPFRDYLR 77
DB 43 LPVYIIVFTTGLGNSVALIMFVPHMRPSGISYVFMNLADFLVTLTALLIFYTN 102
QY 78 RRHMAFGDIPCRVGLFTLAMNRAGSIVFLTVAAADREKVVHHAHVNTISTRVAGIYC 137
DB 103 KTDWIFGDMCKLQRFIFVHNLGSLIFLCTISVHRTGTVVHKLKKNNAVYSS 162
QY 138 TLMALVITL-----GTYVLLLENHLCVQET-----VSCSEFIMESANGWMD 178
DB 163 LVNALVAVIAPILFYSGTGVRNRKTTTCYDTADEYLSYEVYSKCTVEM----- 214
QY 179 IMFQLEFFMPGLIILFCSEFKIWSLRROQLARQARKKATREFIMVAIVITCYLP--- 235
DB 215 -----FCIPFYITLGCYGLIVKALIK--DLNDSPLRRKSIVYIIVLVANVSYLPEHV 267
QY 236 ---SVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMDLPVYFSSSPKFTYNNLKI 291
DB 268 MKTILNLRALDF-QTPQMCAPFNKDYATYQVTRGLASLNSCVPIILYFLAGDFFRRRLSR 326
QY 292 LKICSLKPKOPGHSKTQPREMPISNL 318
DB 327 ATRKSSRSRSEP--NVOSKSEMTLNIIL 351

Search completed: March 26, 2003, 19:44:15
Job time : 36 secs

Thu Mar 27 09:01:05 2003

us-09-942-374-2.rapb



GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 19:35:54 ; Search time 20 Seconds

(without alignments)
1663.126 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853

Sequence: 1 MYNSGCRIBEDTISQVMP.....ANSFQSDGQMDPHYEMH 346

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	880.5	47.5	387	2	169302
2	364	19.6	362	2	S33733
3	362.5	19.6	373	2	JC4162
4	354	19.1	373	2	JC4737
5	343.5	18.5	370	2	JC5549
6	339	18.3	308	2	I50241
7	324	17.5	344	2	T09508
8	320	17.3	373	2	A47556
9	310.5	16.8	420	2	I51667
10	309.5	16.7	363	2	I57940
11	307	16.6	391	2	C41795
12	305.5	16.5	391	2	A41795
13	305.5	16.5	391	2	A39297
14	304.5	16.4	359	2	S15403
15	302.5	16.3	369	2	B41795
16	302	16.3	364	2	J01488
17	302	16.3	399	2	I48705
18	300.5	16.2	369	2	A45291
19	300.5	16.2	369	2	D41795
20	300	16.2	328	2	I55450
21	300	16.2	384	2	A47249
22	300	16.2	428	2	A44021
23	299.5	16.1	369	2	JC2083
24	299	16.1	388	2	JN0605
25	298.5	16.1	418	2	A46226
26	298.5	16.1	432	2	A43448
27	298	16.1	428	2	S30508
28	297	16.0	397	2	S66518
29	296.5	16.0	346	2	S29248

30	296	16.0	359	2	A48857	angiotensin II rec
31	296	16.0	375	2	A54946	P-20-nucleotide re
32	295	15.9	384	2	JC4629	somatostatin recep
33	294	15.9	372	2	I38532	delta opioid recep
34	292.5	15.8	361	2	JC5653	G protein-coupled
35	292	15.8	359	2	JC5498	G protein-coupled
36	291.5	15.7	359	2	JC4425	angiotensin II rec
37	291.5	15.7	359	2	JC2134	angiotensin II rec
38	290	15.7	372	2	S34592	delta opioid recep
39	289	15.6	359	2	JC1104	angiotensin II rec
40	288	15.5	355	2	A45177	chemokine (C-C) re
41	288	15.5	372	2	B48227	delta opioid recep
42	287.5	15.5	365	2	S68208	G protein-coupled
43	287.5	15.5	371	2	JC5796	probable chemokine
44	286.5	15.5	359	2	JH0621	angiotensin II rec
45	286.5	15.5	423	2	JC7677	allatostatin recep

ALIGNMENTS

RESULT 1

169202

G protein-coupled receptor HM74 - human

C:Species: Homo sapiens (man)

C:Date: 12-Aug-1996 #sequence #revision 12-Aug-1996 #text_change 19-May-2000

C:Accession: I69202

R:Nomura, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte

A:Reference number: I54751; MUID:94092629; PMID:7505609

A:Accession: I69202

A:Status: preliminary; translated from GR/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-387 <RES>

A:Cross-references: GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867

C:Genetics:

A:Gene: HM74

C:Superfamily: G protein-coupled receptor 4

Query Match	47.5%	Score 880.5	DB 2	Length 387
Best Local Similarity	52.2%	Pred. No. 5.1e-74		
Matches 178	Conservative 49	Mismatches 107	Indels 7	Gaps 4
QY	5	SCCRREGDTISQVMPDLIVAFVGLGNGVALGCECFHMTKPSVYLLFNLADEFL	64	
DB	17	NCCVFRDDITAKVLPVPLGLGFLIFGLGNGLALMIFCHLSKWSKIFLNLAVADFL	76	
QY	65	MICLPEFTDYLRRRHMAFGDIPCRVGLFTLAMRAGSIVELTVVAADRYKVVPHAV	124	
DB	77	ITCLPEVMDYVRRSDWNGDIPCRVLFMFAMNRQGSIFLTVVAADRYKVVPHAL	136	
QY	125	NHISRVAAIGVCTMALVILGTVYLLLENHLCVOETAVSCSEFIMESANGHDMFDE	184	
DB	137	NKISMTAAIIECLMLGIVGLVHLKLLKLLQNGPANVCISFICHTFRWHEAMFLE	196	
QY	185	FEMPGLIFCFKFIWYSRRROQLARQAMKARFIMVAVITVYLSVARSLEL	244	
DB	197	FLLPGLIIFCSARITWSLRQ-QMDRAKIKRALTFTIMVAIVVIFCLSVVVRKIF	255	
QY	245	KTVPSA--CD-PSVHGHITLSTFYVMSMDPLVLYESSPFPKYNKLKICSLKP	299	
DB	256	WLHTISGTCNCEVYSVDLAFITLSTFYVMSMDPLVLYESSPFPKYNKLKICSLKP	315	
QY	300	KOPGHSKTORPEEMPSINIGRSCISVANFQSDGQMDP	340	
DB	316	KMTGEPDNKRSTSVELTGDPNKT-RGADEALMANSGEPWSP	355	
RESULT 2				
S33733				
G protein-coupled receptor - chicken				
C:Species: Gallus gallus (chicken)				

RESULT 3
P2Y receptor - bovine
JC4162
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Oct-1995 #sequence_revision 10-Nov-1995 #ext_change 24-Sep-1999
C:Accession: JC4162
R:Renderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
B:Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A:Title: Cloning and characterisation of a bovine P2Y receptor.
A:Reference number: JC4162; MUID:95352058; PMID:7626079
A:Accession: JC4162
A:Molecule type: mRNA
A:Residues: 1-373 <HEN>
A:Cross-references: EMBL:X87628; NID:g1032484; PIDD:CA60958.1; PID:g1032485
A:Experimental source: aortic endothelial cell
C:Genetics:
A:Gene: bovy2y
C:Superfamily: ATP receptor P2u
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:52-77/Domain: Transmembrane #status predicted <TM1>
F:88-111/Domain: Transmembrane #status predicted <TM2>
F:124-150/Domain: Transmembrane #status predicted <TM3>
F:171-191/Domain: Transmembrane #status predicted <TM4>
F:214-237/Domain: Transmembrane #status predicted <TM5>
F:261-282/Domain: Transmembrane #status predicted <TM6>
F:305-328/Domain: Transmembrane #status predicted <TM7>
F:11-77,113,197/Binding site: carboxylate (Asn) (covalent) #status predicted
F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.6%; Score 362.5; DB 2; Length 373;

	Best Local Similarity	27.5%;	Pred. No.	6.6e-26;	
	Matches	92;	Conservative	68;	Mismatches 140; Indels 35; Gaps 7;
QY	18	MEPLLIVAVLALNGVALCGECFHHKTKWSTLYLEMLAVADELLMICLPFRDYIYR	77		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	54	LPAVYLIVLVIIIFELGNSVAIMMVFPMKWISIVYMENMLADFLYLTTLTALLIFYFN	113		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
QY	78	RHRMAAFDPCRCVNGJFTLAMNAGSIVFTLVAAABRYFYVPHHNAVINTSRVAAGITC	137		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	114	KIDWIEGDAMCKLQRFIFHVNLXGISILPLTCISAHRSQGVYIPLRSLGLKKKNAYITSV	173		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
QY	138	TLMALVIICTYLLLENHLVCQET-AVSC-----ESFTMESANGMDIMOLFEEFM	187		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	174	LWLVLVVVGISPILFEYSGGIRKRNKTICYDTDSIELHSYFIYSM-----CTVAMFCV	228		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
QY	188	PLGIILFFCFSEFKIYWSLRRRQQLARQARKMKATRFIMVVAIVITPYCLP-----SVAR	240		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	223	PLVLLIGCYGLVRALKLYK-DIDNSPLRKRSIYLIIVLYVFAVSYPHFVHKTNLAKR	287		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
QY	241	IYFLMTVPSSACDPSPHGALHTITLSFTYMSNMIDLVIYYFSPPSKPFYNNKIPICTSLAPK	300		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	288	IDF-QTEPMCACANDRVYAIVYQTRGLASINSCVDPIELFLADGTFRRRLSR-----	337		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
QY	301	QGSHSKTORPEEMPRISNLGRCSISVANFOSQSD	335		
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :			
Db	338	--ATRKASRSEANLOSSESMDTMLTIILEEFGONGD	370		

RESULT

G protein-coupled receptor P2Y1 - human

C;Species: Homo sapiens (man)

C;Accession: JC4737; JC4615; S54253

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A; Reference number: JC4737; MUID:96205320; PMID:8630005

A; molecule type: DN

A; Cross-references: GB:

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A;Reference number: JC4615; MUID:96158962; PMID:8579591

A: Molecule type: mRNA

A/Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
Submitted to the *Journal of Interpersonal Violence* 10/2007

A; Description: Cloning of a human putative P2Y receptor.

A;Accession: S54253
A;Status: preliminary

A:Residues: 1-137 139-373 <TEO>

Cross-references: EMBL:Z49205; NID:g/98835; PIDN:CAA89066.1; PID:g/98836

A:Gene: p2Y1: GDB:P2BY1
C:Genetics:

```
A:Map position: 3inter-3ater
A/cross-references: GDB:6//125; UMLM:60116/
```

Keywords: G protein-coupled receptor

```
E;32-11/Domain: transmembrane #status predicted <TM1>
```

Transmembrane #status predicted	Domain #status predicted	TM4	TM3	TM2	TM1
F:171-191/Domain	transmembrane				
F:124-132/Domain	transmembrane				

	Query Match	17-38:	Score 320:	DB 2:	Length 373:
	Best Local Similarity	30.1%:	Pred. No.	5.9e-22:	
	Matches	98:	Conservative	44:	Mismatches 150; Indels 34; Gaps 8;
OY	4	GSCCRIEGTTISQWMPPLIIAIVFVIGALGNQVALCGCFPHMKTKTWKSTVYLFLNLAADEL	63		
		: :			
Dd	22	GKCRKNDEFEKVLLPVSYGVVCVGLCLNVAALIFLCRLKTWNASTTYMFIHAAVSDSL	81		
OY	64	LMIICPEFTDYILRRRHHAFGDI PCRVGLFTLANNRASGLFTLVVAADYEFKVVPRHHA	123		
		: :			
Dd	82	YAASLPILYYVYARDDHPFSYVLCKLVRLEFTYNLKCSILFELTFCISVHRCGLVPRHS	141		

QY	14	ISGVPELLIAVFEVGLAGNVALCGCFPMKTKMSTYVLFMAVADFLMLCTPEFTD	73
		::: : : : : : : : : : : : : : : : : : : : : : : :	
Db	100	LKREVSLETVYFVIGDELPLNLATILFLFMKKKRAVYMYMLADVEFVSYPLEKIA	159
QY	74	YLLRRHMAFGDIPCRVGLFTLANRAGSIYVFLTVAADRYKVVHPHAAVTVISTRAA	133
		: : : : : : : : : : : : : : : : : : : : : :	
Db	160	YHISGMDLFGGMRITATLFTYCNATCSVLLIASISVDREPLAVVYPMHSIW-RTMSRA	218
QY	134	GIYCT-LMAVLVILGTVLL--ENHLCVQETAVSCSEFI-MESANGMDINFO---LEF	185
		: : : : : : : : : : : : : : : : : : : : : :	
Db	219	YMACSPIMLISIASTIPLWTEQYQIKPRIDITTCHDVLDLMDKDPIYVFFSSCLLF	278
QY	186	FMPGLILFCSEKIYWSIRRHQOLARQARKKATRFIMVAIVFTTC-----YL	234
		: : : : : : : : : : : : : : : : : : : : :	
Db	279	FVPFIITTCYIGIIRSL-SSSSIENSCSKTRALLPFAVWLCVEFIICGPTNVLEFPHL	337
QY	235	PVSARLEFLMTVYSSADDVSHGALHITLSFTYAMSMDPLVYVFFSSPEPKYMKIKI	294
		: : : : : : : : : : : : : : : : : : : : :	
Db	338	QPANELLEFAVIL--SACVGV-----SCCLDPLIYYAASSOCQRYLYSL-L	384
QY	295	CSLKPQGHGSKTQ	308
		: : : : : : : : : : : : : : : : : : : :	
Db	382	CCRAKVSFGSGSTGQ	395

somatostatin receptor 5 - rat
 Walthermate names: somatostatin release-inhibiting factor subtype 28 receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Nov-1999
 C:Accession: I57940: I57949: S39244
 R:O'Carroll, A.M.; Iohat, S.J.; Konig, M.; Mahan, L.C.
 Mol. Pharmacol. 42, 939-946, 1992
 A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with F

Query Match	16.7%;	Score 309.5;	DB 2;	Length 363;
Best Local Similarity	29.6%;	Pred. No. 5.4e-21;		
Matches 96;	Conservative 53;	Mismatches 148;	Indels 27;	Gaps 9;

RESULT 11

;Cross-references: GB:M81831; NID:g201058; PIDN:AAA58255.1; PID:g201055
;Superfamily: vertebrate rhodopsin

Query Match	16.68;	Score 307;	DB 2;	Length 391;
-------------	--------	------------	-------	-------------

310 ILGYANSCANPILYGFLSDNFKRSFQRI-LC 339

1 - human somatostatin receptor

```
;339/Binding site: palmitate (Cys) (covalent) #status predicted
```

```
query match      16.5%; score 305.5; db 2; length 391;
```

Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;

b 47 QNGTSEGGSAILLSFYSSVCLVGLGNSMVIYVILRYAKMKTATNIYILNLAIADEL 106

```

OY      64  IMICPFETDYLLRRRRHMAFDICRGFETLLAMNRAGSIYFETLYVAABRYEFVHPHHA 123
      || : :|| || : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :||
Db      107  LMLSPLELYVSTL-LRRHMPGALLCRLLVSDVADNMMTSTYTCITLVSDRYAAVHPHRA 165
OY      124  VNTISTRVAAGICTLMAALVILGTVYLLENHLCV-OETAVSCSEFIMESANGMD--- 178
      || : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :||
Db      166  ARYRPRTAKVAVNGVWVLSLLVILPIYVSRTAANSDDGTVAACNMIMPEAPQRMLGEVYL 225
OY      179  IMFOLEFPMPGILIFLC-----SPKIYWSLRRROQLARQRMKARFELIVVAI 227
      | : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :||
Db      226  YTFLLAGFLLPYGAICLCYVILIAKMRVALLAKGQQRKSE-----KRTILMVAVVVA 278
OY      228  VFITCYLPSVSARLYFLMTVPSSACDPSVGALHILTFYVNSMMDPLVYFYFSSPSPEK 287
      || : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :|| : :||
Db      279  VFVICMMFPEYVVLAVNFAEDDQDAT-----VSQLSVILGYANSKANPILYGLSDNFR 332
OY      288  FYNNKLTIC 295
      : : :|| :
Db      333  SFQRI-LC 339

```

RESULT 13

N:Alternatename: probable G-protein-coupled receptor: SKRF receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
 C:Accession: A39297; A45102; S20088
 R:Mejertorf, W.; Paust, H.-J.; Schoenrock, C.; Richter, D.
 RNA Cell Biol. 10, 689-694, 1991
 A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed
 A:Reference number: A39297; MUID:92096119; PMID:1661599
 A:Accession: A39297
 A:Molecule type: mRNA
 A:Residues: 1-391 <MEY>
 A:Cross-references: GB:X62314; GB:X61630; NID:g56309; PIDN:CA44193.1; PID:g55310
 A:Experimental source: brain
 A:Note: It is uncertain whether Met-1 is the initiator or whether translation is initiated
 R:Li, X.-J.; Forte, M.; North, R.A.; Ross, C.A.; Snyder, S.H.
 J. Biol. Chem. 267, 21307-21312, 1992
 A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
 A:Reference number: A45102; MUID:93016064; PMID:1400442
 A:Accession: A45102
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-391 <LI1>
 A:Experimental source: brain
 A:Note: sequence extracted from NCBI backbone (NCBI:116692)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

Query Match	16.5%;	Score 305.5;	DB 2;	Length 391;
Best Local Similarity	26.3%;	Pred. No. 1.4e-20;		
Matches 81;	Conservative 62;	Mismatches 128;	Indels 37;	Gaps 8;

QY 10 EGDRTISQYMPPELLLYIAEY-----IGALGVNVALCGCEFHKKTWKPSVYLYEFLNVAADF 63
 Db 47 QNGTISEQGSAILLSTFYISVYCVLGVLCGNSMAYIYLLIRAKMTATINITYLNATIDEL 106
 QY 64 LMICLPETDYILRRRHAFGDICRVLGFTLANNRAGSIVELTVADRYEKVYVHHNA 123
 Db 107 LMLSVPLVLTSTL-LRRHPGALLCRILVSDAVNMFTSYICLVAFISVDRYVAVHPDIA 165
 QY 124 VNTISTRVAALICTMALVILGYVLLLEHNLGV-OETAVSCSSTFMESANGHND---- 178
 Db 166 ARTRRPYAKVNLGVWVLSLVLITLIVFERTSANGDGVACMLMLPEPQRLVGEVL 225
 QY 179 IMFOLFEPMPGILIFC-----SFRIVMSLRROOLARQAMRKATRPILVVAI 227
 Db 226 YTFPLMGFLPLPVGALCICVYLIIAKMRVWALKAGNOQKRSE-----RKITLVMNVVM 278
 QY 228 VFTICLYPVSARLYELMTVPSSACODPSVGHALHTLSFTYMNMSMDPLVYFESSPSFPK 287

Db	279	VFFVLCMMFFVYVQLVNFVFAEDDDAT-----VSQLSYILGLANSANCPILYGLFSDNFKR	332
Qy	288	FYNKRLKIC	295
Db	333	SFQRI-LC	339

RESULT 14

angiotensin II receptor type 1 - bovine
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C:Accession: S15403
 R:Sasaki, K., Yamano, Y., Bardhan, S., Iwai, N., Murray, J.J., Hasegawa, M., Matsuda,
 Nature 351, 230-233, 1991
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angio-
 A:Reference number: S15403; MUID:91251900; PMID:2041569
 A:Accession: S15403
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
 C:Superfamily: vertebrate rhodopsin

Query Match	16.4%	Score 304.5;	DB 2,	Length 359;
Best Local	24.9%;	Pred. No. 1.5e-20;		
Matches 81;	Conservative 68;	Mismatches 143;	Indels 33;	Gaps 8

```

QY      17  VMPRLIIAFLAFLALGNGVALACGCFMCKTTPSTVYLFLVAADFLMLICLPRDTYYL  76
      18  :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      30  MIPFLYSIIIFVVGIFGNSLIYIYIFFMKLTVASFLLMLALADCELLTLPMLANYTA  89

QY      77  RRRHWAQGDIPCRVGLFTLMMNRAGSIVETLVAADRIKFKVNHHAUNFTISRVAAGIV  136
      78  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      90  MEYRMPPEPNYCKLASASVSFNLASVFLTLCLSDIYDLIVHBMKS-RLRRTMLVAKYT  148

QY      137  C-TMALVLIITGVLLL-ENHLGQVFAVSCSEFIMESANGMHIMOLE-----FPMPL  189
      138  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      149  CIIIMWLAGLASLEPTIIHRNFEIENITNIPGCAHYESQNSLTPVGLGIRKNILGLFPE  208

QY      190  GIILFCSEKIYMSLRROQLARQARMKKATREIMVAYI--FITCIYLP-----SYSANLYF  243
      191  :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      209  -LIITSTYLLIMKLKRAYEIQKKPKRDKFIILAIVFFPSSWPHOIFTFMDVLIO  267

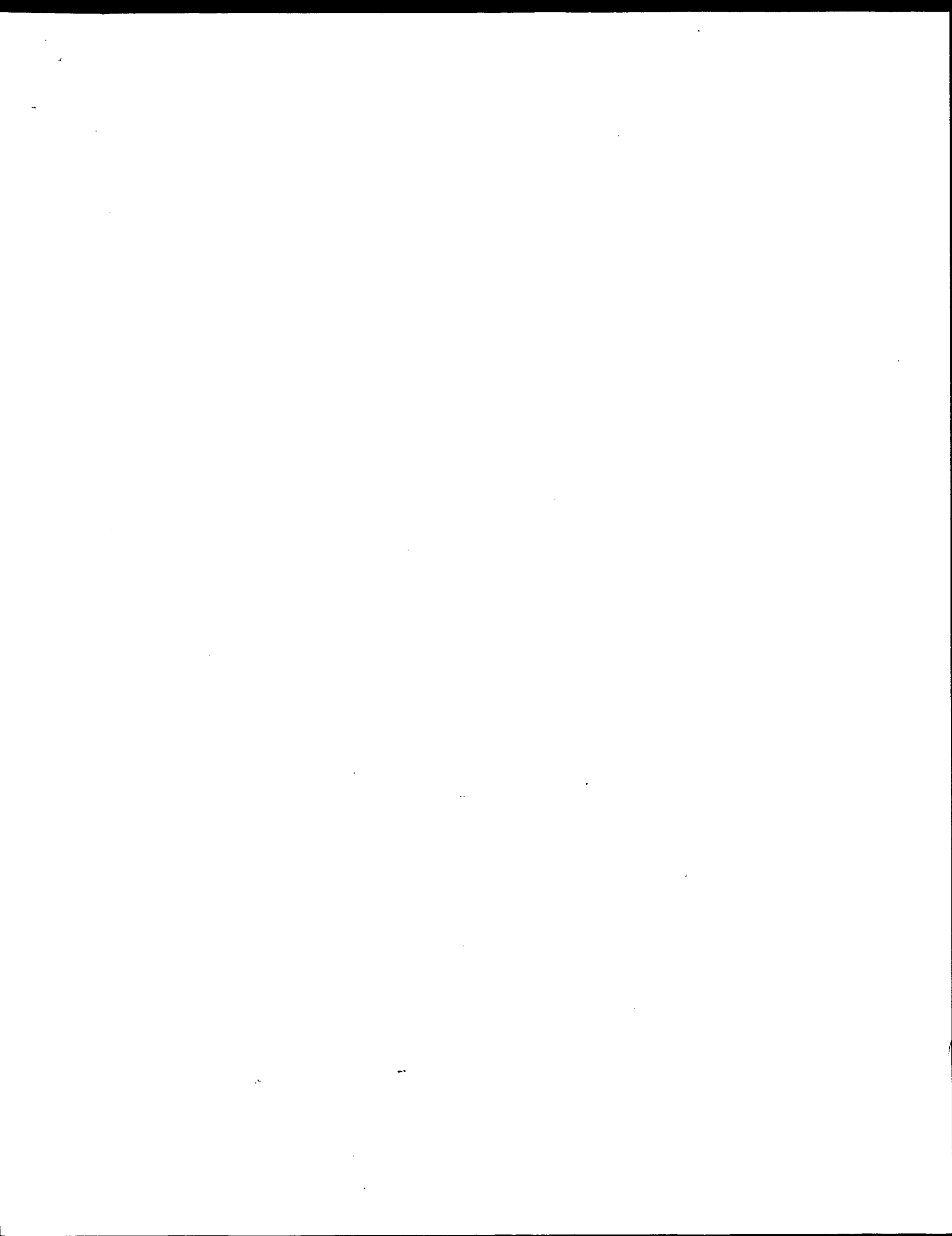
QY      244  LMTVPSSACDPVSVAIHTLISFYNNMSMDPLVYYFSSSEFPKEY-----289
      245  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      268  LGLIRDCKIEDIYDTPMPTICIAIYFNNCUNLPLELYGLGRKKFKYFLQLLKTIYPRKASH  327

QY      290  ----NKLKICSLAKPOGSHSTQNP  310
      291  |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      328  SNLSTKMSLTLSYRPSNGNSSTKKP  352

```

RESULT
B41795

somatostatin receptor 2 - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
 C:Accession: B41795
 R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Setino, S.
 Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
 A:Title: Cloning and functional characterization of a family of human and mouse somatostatin receptors
 A:Reference number: A41795; MUID:92108031; PMID:1346068
 A:Accession: B41795
 A:Molecule type: DNA
 A:Residues: 1-369 <YAM>
 A:Cross-references: GB:881830; NID:g307435; PIDB:AAA58248.1; PID:g307436
 A:Note: sequence extracted from NCBI backbone (NCBIN:74769, NCBIPI:74770)
 C:Genetics:
 A:Gene: GDB:SSFR2
 A:Cross-references: GDB:134186; OMIM:182452
 A:Map position: 17q24-17q24



DR	PROSITE: PS00237; G_PROTEIN_RECIP_FL1; 1.
DR	PROSITE: PS00262; G_PROTEIN_RECIP_FL2; 1.
KM	G-protein coupled receptor; Transmembrane.
FT	DOMAIN 1 16
FT	TRANSMEM 17 37
FT	DOMAIN 38 52
FT	TRANSMEM 53 73
FT	DOMAIN 74 91
FT	TRANSMEM 92 110
FT	DOMAIN 111 131
FT	TRANSMEM 132 152
FT	DOMAIN 153 180
FT	TRANSMEM 181 201
FT	DOMAIN 202 219
FT	TRANSMEM 220 240
FT	TRANSMEM 241 265
FT	TRANSMEM 266 284
FT	DOMAIN 285 319
FT	CARBOHYD 5 5
FT	SEQUENCE 319 AA; 35079 MW; 74AF164CD9C969DD CRC64;
Query Match	24.2%; Score 448.5; DB 1; Length 319;
Best Local Similarity	34.0%; Pred. No. 2e-24;
Matches 100; Conservative 62; Mismatches 121; Indels 11; Gaps	
QY	7 CRIEDRTISQVMPRLIYAFLVGLANGVGLGFCFENHKTWPKSTVYFENLAVDFLMI 66
DB	6 CSAPSTVATAGVGLVLEGCGILGNVNLMTLEFRVWKMPYAVYVNLNLADLLLA 65
QY	67 CLPFTDYLYRRHNAFQDIPCRVGLFTLLAMRACISIVFLYVADRFKVVPHNAVY 126
DB	66 CLPFAAYFLSLQAHNLGRVGCWALRFLLDLSRSGMFAFLAVNALDRYLRRVHPRLKYNL 125
QY	127 ISTRVAAIVCTLMALVILITGVYLLLENNLCVOETAVSCSEPTMESANG----WHDLMF 181
DB	126 LSPQALAEVSGVWMLLMALNCPGLLIE--AAQNSTCHSF-YSRAGDSPTIQQEALS 182
QY	182 QLEFMPYLGIILFCSEFKTWSILRR-QQLARQARKKATRFIMVAVIFTCYLPVSAR 240
DB	183 QLEFMPYLGIILFCSEFKTWSILRR-QQLARQARKKATRFIMVAVIFTCYLPVSAR 240
QY	241 --IVFLMWVPSACDPSVHGALHILSTFYNNMSMLDPLVYVFSSSPFKFYNKL 292
DB	243 VLMHIFQNLGSRALCAVAHTSDVTGSLTYLHVSVPVAVYCPSSPFFRSYRRV 296

OS CYSLTR2 OR CYSLT2 OR CYSLT2R.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=20374466; PubMed=10913337;
 RA Takaasaki J., Kanohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
 RA Nishikawa T., Kawai Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,
 RA Furuchi K.;
 RT "The molecular characterization and tissue distribution of the human
 RT cysteinyl leukotriene receptor.";
 RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20458128; PubMed=10851239;
 RA Helise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
 RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
 RA Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
 RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
 RA Lynch K.R., Evans J.F.;
 RT "Characterization of the human cysteinyl leukotriene 2 receptor.";
 RL J. Biol. Chem. 275:30531-30536(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20545741; PubMed=11093801;
 RA Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
 RA Civelli O.;
 RT "Molecular cloning and characterization of a second human cysteinyl
 RT leukotriene receptor: discovery of a subtype selective agonist.";
 RL Mol. Pharmacol. 58:1601-1608(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RN Dunn M.;
 RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 17-346 FROM N.A.
 RA Suga H.;
 RT "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system. Stimulation by BAY u9773, a
 CC partial agonist, induces specific contractions of pulmonary veins
 CC and might also have an indirect role in the relaxation of the
 CC pulmonary vascular endothelium. The rank order of affinities for
 CC the leukotrienes is LTC4 = LTD4 > LTE4.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
 CC gland. In lung, expressed in the interstitial macrophages, and
 CC slightly in smooth muscle cells.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: AB038269; BAB03601.1; -;
 DR EMBL: AF254664; AAG17281.1; -;
 DR EMBL: AF279611; AAK69485.1; -;
 DR EMBL: AL137118; CAC29102.1; -;
 DR EMBL: AB041644; BAB16379.1; -;
 DR MIM: 605666; -;
 DR InterPro: IPR004071; CysLeuk_receptor.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PRO1533; CYSLTRECPT.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1.1; FALSE_NEG.
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT DOMAIN 64 72
 FT TRANSMEM 73 93
 FT DOMAIN 94 123
 FT TRANSMEM 124 144
 FT DOMAIN 145 153
 FT TRANSMEM 154 174
 FT DOMAIN 175 204
 FT TRANSMEM 205 225
 FT DOMAIN 226 245
 FT TRANSMEM 246 266
 FT DOMAIN 267 286
 FT TRANSMEM 287 307
 FT DOMAIN 308 346
 FT DISULFID 111 187
 FT CARBOHYD 20 20
 FT CARBOHYD 26 26
 FT CARBOHYD 30 30
 FT CARBOHYD 181 181
 SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DCE3EE4 CRC64;

Query Match 19.8%; Score 366.5; DB 1; Length 346;
 Best Local Similarity 29.9%; Pred. No. 1e-18;
 Matches 94; Conservative 69; Mismatches 134; Indels 17; Gaps 8;

QY 3 NSGCCAIEDDTISQVMPPLIYAFVYALGNGVALCGFCFHMKTWPKST--VYLFNLAV 59
 DB 27 NSNRKITE-NKREKPPYLLIIFEWGVLGNGSIYVF--LQPKKSTSVNVMNLAI 82
 QY 60 ADELIMICPFRTDYDYLRRHNAFGDIPCRVGLFTLMMRASIYFLTVAADRFKVVH 119
 DB 83 SLLFLSTLPFRADYLRKSNMIFGDLAKRISYSLYVMSSYFLVLSVRFAMVH 142
 QY 120 PHHAVTISTRAAGIVCTMALVLTGYLLLENHLCVOETAVSC--ESFIMESANGW 176
 DB 143 PERLHVTSIR-SAMILCGIIMLIMWASSIMLDSGSENGSVTSCLELTKIAKLTQM 201
 QY 177 HDIMPLEFFMPLGIIIFCSFKIWSLRKQ--QLARQARKAKATRFIMVAVITCYL 234
 DB 202 NTAIALVVGCLPFTLSICYLLIIRVLKVEVEGSLRVSHRKALTTIITLIIFLCPL 261
 QY 235 PSVSARLYFLMTVPSSACDPVSHGALHILTSFYMSMDPLVYFESSPSEKFKYNTKI 294
 DB 262 PYHTLFTVLTWKVGLCKDRHLKALVITLALANACNPILTYFAGENK--DRUK- 317
 QY 295 CSLKPKOPGHSKTQ 308
 DB 318 SALRKGHPOKAKTK 331
 RESULT 5
 P2YR_CHICK STANDARD: PRT: 362 AA.
 AC P3496;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
 GN P2YR1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

RX MEDLINE=93285340; PubMed=8508924;
 RA Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
 RA King B.F., Burnstock G., Barnard E.A.;
 RT "Cloning and functional expression of a brain G-protein-coupled ATP
 RT receptor.";
 RL FEBS Lett. 324:219-225(1993).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RA MEDLINE=97026278; PubMed=8872457;
 RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
 RT "Modelling the P2Y purinoceptor using rhodopsin as template.";
 RL Drug Des. Discov. 13:133-140(1995).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
 CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERUSSIS TOXIN
 CC INSENSITIVE G-PROTEIN. PROBABLY BELONGING TO THE GQ FAMILY THAT
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,
 CC STOMACH, LUNG AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC EMBL: X73268; CA51716.1; -.
 CC PIR: S33733; S33733.
 CC DR PDB: 1DDO; 11-JUL-96.
 CC DR InterPro: IPR000276; GPCR_Rhodopsin.
 CC DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PRO0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1.1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECEPTOR_F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
 FT DOMAIN 1 41
 FT TRANSMEM 42 63
 FT DOMAIN 64 76
 FT TRANSMEM 77 98
 FT DOMAIN 99 115
 FT TRANSMEM 116 136
 FT DOMAIN 137 155
 FT TRANSMEM 156 177
 FT DOMAIN 178 207
 FT TRANSMEM 208 227
 FT DOMAIN 228 254
 FT TRANSMEM 255 274
 FT DOMAIN 275 292
 FT TRANSMEM 293 317
 FT DOMAIN 318 362
 FT DISULFID 113 191
 FT CARBOHYD 11 11
 FT CARBOHYD 26 26
 FT CARBOHYD 102 102
 FT CARBOHYD 186 186
 SQ SEQUENCE 362 AA; 41194 MW; A80C88FB9514761 CRC64;

Query Match 19.6%; Score 364; DB 1; Length 362;
 Best Local Similarity 29.1%; Pred. No. 1.5e-18;
 Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

QY 18 MPPLIYAFVYALGNGVALCGFCFHMKTWPKSTVYLFNLAVADFLMCLPRTDYLR 77
 DB 43 LPTVYLLVFTTGLGNSVAITMVEFHMWPWSGISYVMFNALADFLYVLTLPALIFYRN 102
 QY 78 RHHAFGDIPCRVGLFTLANNRAGSIVFLTVAADRFKVVHHAHVNTISTFAAGIYC 137
 DB 103 KTDWIFGDVCKLQRFLEHVNLYGSLIFLTGISVHRYGVVHPLKSLGRKKNAVYSS 162

FT	TRANSMEM	42	63	1 (POTENTIAL).
FT	DOMAIN	64	76	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	67	98	2 (POTENTIAL).
FT	DOMAIN	99	115	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	116	136	3 (POTENTIAL).
FT	DOMAIN	137	155	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	156	177	4 (POTENTIAL).
FT	DOMAIN	178	207	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	208	227	5 (POTENTIAL).
FT	DOMAIN	228	254	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	255	274	6 (POTENTIAL).
FT	DOMAIN	275	292	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	293	317	7 (POTENTIAL).
FT	DOMAIN	318	362	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	113	191	BY SIMILARITY.
FT	CARBOHYD	11	11	N-LINKED (GLICNAC. . .) (POTENTIAL).
FT	CARBOHYD	26	26	N-LINKED (GLICNAC. . .) (POTENTIAL).
FT	CARBOHYD	102	102	N-LINKED (GLICNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLICNAC. . .) (POTENTIAL).
SQ	SEQUENCE	362 AA:	41180 MW; 3EL28AB9EB64349C CRC64;	
Query Match				
Best Local Similarity		19.6%;	Score 364;	DB 1; Length 362;
Matches		95;	Conservative	58; Mismatches 130; Indels 44; Gaps
QY	18	MBPLLIVANFVIGALDNGVALCGCFCHMKRWKRSYLYLFNLAVADFLMICLPEFRDYLYR	77	
DB	43	LPTVILVFETFLGNSVAIMFVHFMRWSGISVYMENLADLRYLLTFLALFYEFN	102	
QY	78	RHRMAFEDIPICVVGLETTAMNRAGSIVFETVVAADRYFVFNPHNAVNTISPRVAIGVC	137	
DB	103	KIDWIEGDMCKLQRFIFRHNLYGSLIFELTCISVIRTYGVNHPKLKSKKKNVYSS	162	
QY	138	TILVALYL-----GTVYLLENHLCOVETA-----VSCSEFIMESANGMHD	178	
DB	163	LMVALVAVAVIADILFYSGGVGRNRKNTITCYDPTADEYLRKYVYSMCTVF	214	
QY	179	IMFOLEFFMPLGIILFCSFKIYWSLRROQLARQARMKATRFINWVAIVFTCYLP---	235	
DB	215	-----FCFPEFYLICGGLIKALIKR-DLDNSPLRKSILYLYITLVFAVSLPRHV	267	
QY	236	-----SVSARLYFLMTVPSSACDPVYGHALHTLTSFYNNMMDPLVYVYSSSPFKPKYK	291	
DB	268	MKTLMRLARLDF-QPRQMCAPFNDKYYATVQVYRGLASINSCVDPIFLYAGDTFRRLSR	326	
QY	292	LKICSLKPKOPGSKTORPEEMPTNL	318	
DB	327	ATRKSRSRSP--NWQSKSEKNTNLL	351	
RESULT 7				
ID	P2YR_BOVIN	STANDARD;	PRT;	373 AA.
AC	P48042:			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	P2Y purinoceptor 1 (ATP receptor) (p2y1) (Purinejergic receptor).			
GN	P2RY1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Arctic endothelium;			
RC	MEDLINE=95352058; PubMed=7626079;			
RA	Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Daitly I.A.;			
RA	"Cloning and characterisation of a bovine P2Y receptor";			
RL	Biochem. Biophys. Res. Commun. 212:648-656(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			

RC TISSUE-Corpus callosum;
 RX MEDLINE=99064562; PubMed=9848096;
 RA Deng G., Maute C., Kumar C., Fogarty D.J., Miledi R.;
 RT "Cloning and expression of a P2y purinoceptor from the adult bovine
 corpus callosum.";
 RL Neurobiol. Dis. 5:259-270(1998).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
 CC ATP AND ADP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X87628; CAA60958.1; -;
 DR EMBL: U34041; AAC78275.1; -;
 DR HSSP: P34996; IDDD
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
 DR PROSITE: PS0262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 53 74 1 (POTENTIAL).
 FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 88 109 2 (POTENTIAL).
 FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 127 147 3 (POTENTIAL).
 FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 188 4 (POTENTIAL).
 FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 219 238 5 (POTENTIAL).
 FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 266 285 6 (POTENTIAL).
 FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 304 328 7 (POTENTIAL).
 FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 124 202 BY SIMILARITY.
 FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 373 AA; 42287 MW; 9270A7175C0BDA76 CRC64;
 Query Match 19.6%; Score 362.5; DB 1; Length 373;
 Best Local Similarity 27.5%; Pred. No. 2e-18;
 Matches 92; Conservative 68; Mismatches 140; Indels 35; Gaps 7;
 QY 18 MPELLIVAVLCAALNGVALCGFCFHMKTWKPSTVYLFNLAVADLMLICLPFRIDYLR 77
 DB 54 LPAVYLVVIFELFGLNSVAIMFVPHMKPWSGISVYMFLADLPLVLLPALLFYEN 113
 QY 78 RRMHAGDIPRCVGLFTLMMNRAGSIVFLTVAAADRYFVPHHAIVTSIRVAGIYC 137
 DB 114 KIDMIFGDMACKIQRIFIVHNLXGSLFLTCTSAHRYSSVYPLSLGKTKKNVYISV 173
 QY 138 TMAVVIIGTVYLLLENHLCVQET-AVSC-----ESFTMESANGMDIMFQLEFEM 187
 DB 174 LVMLIVVAGISPLIFYSFGIRKRNKTIICYDTTSDLYLSFIYSM-----CTVAMFCV 228
 QY 188 PLGIIIFGCFKIVYSRRQQLARQARKKATRFIMVAIVITCYLP-----SVGAR 240
 DB 229 PLVLIGCGGLVRLALIV-DLDNSPLRKRSIYLVILVFAVSYIPFHVWKMLRAR 287
 QY 241 LVFLMTVPSSACDPVSHAGLHITLSPFYNSMLDPLVYVYFSSPSPKFKYKLIKCSLKP 300
 pb 288 LDF-QTPEKCAFRDRIYATYQVTRGLASLNSCVDPLIVFLAGDTTFRRLSR----- 337

QY 301 QPCHSKTQREEMPISNLGRSCISVANSFQSGSD 335
 DB 338 -ATKRRSRSEANLQSKSEMDTLITLSEKONGD 370
 RESULT 8
 CLUT2_PIG
 ID CLUT2_PIG STANDARD; PRT; 345 AA.
 AC Q95N03;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Cysteinyln leukotriene receptor 2 (CysLTR2).
 GN CysLTR2 OR CysLTR2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kamohara M., Takasaki J., Matsumoto S., Saito T.,
 RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
 RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
 RT receptors.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB052662; BAB60817.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; FALSE_NEG.
 DR PROSITE: PS0262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 64 1 (POTENTIAL).
 FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 74 94 2 (POTENTIAL).
 FT DOMAIN 95 124 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 125 145 3 (POTENTIAL).
 FT DOMAIN 146 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 175 4 (POTENTIAL).
 FT DOMAIN 176 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 5 (POTENTIAL).
 FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 247 267 6 (POTENTIAL).
 FT DOMAIN 268 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 345 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 112 188 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 345 AA; 39410 MW; 5D1B1FB89B95905 CRC64;
 Query Match 19.5%; Score 362; DB 1; Length 345;
 Best Local Similarity 31.3%; Pred. No. 2e-18;
 Matches 86; Conservative 59; Mismatches 118; Indels 12; Gaps 5;
 QY 19 PELLIVAVLCAALNGVALCGFCFHMKTWKPST-VYLFNLAVADLMLICLPFRIDY 75

FT	TRANSMEM	219	238	5 (POTENTIAL)		
FT	DOMAIN	239	265 <td>CYTOPLASMIC (POTENTIAL)</td> <td></td>	CYTOPLASMIC (POTENTIAL)		
FT	TRANSMEM	266	285 <td>6 (POTENTIAL)</td> <td></td>	6 (POTENTIAL)		
FT	DOMAIN	286	303 <td>EXTRACELLULAR (POTENTIAL)</td> <td></td>	EXTRACELLULAR (POTENTIAL)		
FT	TRANSMEM	304	328 <td>7 (POTENTIAL)</td> <td></td>	7 (POTENTIAL)		
FT	DOMAIN	329	373 <td>CYTOPLASMIC (POTENTIAL)</td> <td></td>	CYTOPLASMIC (POTENTIAL)		
FT	DISULFID	124	202	BY SIMILARITY		
FT	CARBOHYD	11	11	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL)		
FT	CARBOHYD	197	197	N-LINKED (GLCNAC. . .) (POTENTIAL)		
SO	SEQUENCE	373 AA:	42321 MW:	6DDF676287B5E648 CRC64;		
Query Match						
Best Local Similarity		19.3%:	Score 358.5:	DB 1:	Length 373:	
Matches 91:		Conservative	68:	Mismatches 139:	Indels 39:	Gaps
QY	18	MPPLIYAEFLGALGNGVALGCGFCFHMKTWPKSTYVLEENLAVADFLMLTCLPFTDYLR	77			
Dd	54	LPAYVILVFLIGFLGNSVAIMFVFMKPMWSGISVYMNLAADFLVILPLPALLEFYEN	113			
QY	78	RHRHAGEDIPCRGGLTTLAMNAGSIVELTYVADRYKVVPHHAVNTISTRYAAGIYC	137			
Dd	114	KTWIMEDVWCKLQRIEFLHVNLYGSLFELTCLSAHRYSGVYPLKSLGRKKNAIVSV	173			
QY	138	TWALVILGVYLLLENHLCVOET-AVSC-----ESPTMESANGWHDIMFQLEEFM	187			
Dd	174	LWHLIYVVAISPLIFPISGIGIKKNTVCYDSTDEYIRLFTISM-----CTTVAMFCI	228			
QY	188	PLGILIFCSEKIVWSLRRQOLARQARKKATRFIMVAVITICLP-----SVSR	240			
Dd	229	PLVILIGCYGLIYRALIYK-DIDNSPLRKRKSIYIIVILVFEAVSIIPFHMKTMLRAR	287			
QY	241	LYELMTVPSSACD-PSVHGALHILSTFYNSMGLPLYFYFSSPPKRYKNIKLCISLK	298			
Dd	288	LDF-----QTPMCCDFNDRYATYQVTRGLASLNSCDDPLLYFLADDTFRRLSLR-----	337			
QY	299	PKOPGSKTQRPPEMPISMLGRRCISVANSFSOSQD	335			
Dd	338	-----ATRKASRRSEANLQSKSEEMTLNLTSEKQNGD	370			
RESULT 10						
ID	CLUT2_RAT	STANDARD:	PRT:	309 AA.		
AC	0924T9:					
DT	15-JUN-2002 (Rel. 41, Created)					
DT	15-JUN-2002 (Rel. 41, Last sequence update)					
DT	15-JUN-2002 (Rel. 41, Last annotation update)					
GN	Cysteinyl leukotriene receptor 2 (CysLTR2) (RSPB372).					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,					
RA	Omishi T., Soga T., Matsushime H., Furuchi K.;					
RT	Characterization of the cloned rat and porcine cysteinyl leukotriene					
RT	receptors *;					
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.					
CC	-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is					
CC	mediated via a G-protein that activates a phosphatidylinositol-					
CC	calcium second messenger system (By similarity).					
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.					
CC	-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.					
CC	-----					
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CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					

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CC -----

DR EMBL: AB052661; BAB60816.1; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; FALSE_NEG.

DR PROSITE: PS0262; G_PROTEIN_RECIP_FL_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 26

FT TRANSMEM 27 47

FT DOMAIN 48 56

FT TRANSMEM 57 77

FT DOMAIN 78 98

FT TRANSMEM 99 119

FT DOMAIN 120 137

FT TRANSMEM 138 158

FT DOMAIN 159 187

FT TRANSMEM 188 208

FT DOMAIN 209 229

FT TRANSMEM 230 250

FT DOMAIN 251 271

FT TRANSMEM 272 292

FT DOMAIN 293 309

FT DISULFID 95 171

FT CARBOHYD 14 14

FT CARBOHYD 166 166

FT CARBOHYD 167 167

SO SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 19.2%; Score 355.5; DB 1; Length 309;

Best Local Similarity 31.2%; Pred. No. 5.2e-18;

Matches 91; Conservative 57; Mismatches 131; Indels 13; Gaps 7;

OY 2 YNSCCRIGSDITISQMPPLLIAPVLGALGNGVALGCGCFEMKWKST---VYLFNLA 58

DB 10 YSKNCTIE-NKRDFFPIYILIFVWGLNGSGIYF---LQYKKSTVYVVEMLNLA 65

OY 59 VADFLLMCLPRTDYLLRRHMAFGDIPCRGLFTLANRAGSIYFLTVVADRYFKV 118

DB 66 ISDFLISLPRADVNFSGDMIGDMACRIMSYSLVNMSTIYFLTVLSIVAFMTA 125

OY 119 HPHHAVNTISTRYVAGIVC-TLMALVILGTVYLLLENLHLCVOEIVAVSCSEFTMESAN--G 175

DB 126 HFOQMHLITSVR-SAWIILGIIWVFIWMASSGLLKHGQKKNNKTLCFELNLQKFKNVI 184

OY 176 WHDIQMLPEPMPGLITLCSFKIWSLRRRO--QLARQARKKATRFIMVAIVETICY 233

DB 185 LNTIALGVFLPFIITLTCYLLILRVLLKVEIPESGPRDQKALTTIVIMTIFLLCF 244

OY 234 LPSVSARLYFLMTVPSSACDPVHGALHTLSFTYNSMLADPVLVYFSSPSF 285

DB 245 LPHHALRTHLVWMDSCMDLHKATVITLLAANSCFNFLVYFAENF 296

RESULT 11

ID P2YR_HUMAN STANDARD; PRT; 373 AA.

AC P47900;

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).

GN P2RY1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=96257237; PubMed=8666290;

RA Leon C., Vial C., Cazenave J.-P., Gachet C.;

RT "Cloning and sequencing of a human cDNA encoding endothelial P2Y1 purinoceptor.";

RT Gene 171:295-297(1996).

RL [12]

RN SEQUENCE FROM N.A.

RP MEDLINE=96158962; PubMed=8579591;

RX Ayanathan K., Tanta W., Harbansjit S., Raghbir A.S., Barnard E.A., Kunapuli S.P.;

RA "Cloning and chromosomal localization of the human P2Y1 purinoceptor.";

RT Biochem. Biophys. Res. Commun. 218:783-786(1996).

RL [13]

RN SEQUENCE FROM N.A.

RP MEDLINE=96205320; PubMed=8630005;

RX Janssens R., Communi D., Piroton S., Samson M., Parmentier M., Boynaems J.M.;

RA "Cloning and tissue distribution of the human P2Y1 receptor.";

RL Biochem. Biophys. Res. Commun. 221:588-593(1996).

RL [14]

RN SEQUENCE FROM N.A.

RP TISSUE=Blood;

RL Leon C., Vial C., Cazenave J.-P., Gachet C.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RL [15]

RN SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.

RP TISSUE=Platelet;

RC MEDLINE=9813162; PubMed=9442040;

RX Jin J., Daniel J.L., Kunapuli S.P.;

RA "Molecular basis for ADP-induced platelet activation. II. The P2Y1 receptor mediates ADP-induced intracellular calcium mobilization and shape change in platelets.";

RT J. Biol. Chem. 273:2030-2034(1998).

CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION OF INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C. A CHANGE IN PLATELET SHAPE, AND PROBABLE TO PLATELET AGGREGATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC A3P5PS, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION AND SHAPE CHANGE IN PLATELETS.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: Z49205; CAA89066.1; -

DR EMBL: U42030; AAA97873.1; -

DR EMBL: U42029; AAA97872.1; -

DR EMBL: S81950; AAB47091.1; -

DR EMBL: AJ006945; CAA07339.1; -

DR EMBL: AF018284; AAB94556.1; -

DR HSSP: P34966; 1DD.

DR Genew: HGNC:8539; P2RY1.

DR MIM: 601167; -

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS00237; GPCR_Rhodpsn.

DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.

DR PROSITE: PS0262; G_PROTEIN_RECIP_FL_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;

KW Blood coagulation.

FT DOMAIN 1 52

FT TRANSMEM 53 74

FT DOMAIN 75 87

FT TRANSMEM 88 109

FT DOMAIN 110 126

FT TRANSMEM 127 147

FT DOMAIN 148 166

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

```

CC      OF EXTRACELLULAR ATP ON INSULIN SECRETION.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      or send an email to license@isb.slb.ch).
CC
DR      EMBL; U22829; AAA91302.1; -.
DR      EMBL; AJ245636; CAB57317.1; -.
DR      HSSP; P34996; 1DD.
DR      MGd; MG1:105049; P2ry1.
DR      InterPro; IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHHODPSN.
DR      PROSITE; PS00262; G_PROTEIN_RECPE_FL_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECPE_FL_2; 1.
KW      G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT      DOMAIN 1 52
FT      TRANSMEM 53 74
FT      TRANSMEM 75 87
FT      TRANSMEM 88 109
FT      TRANSMEM 110 126
FT      TRANSMEM 127 147
FT      TRANSMEM 148 166
FT      TRANSMEM 167 188
FT      TRANSMEM 189 218
FT      TRANSMEM 219 238
FT      TRANSMEM 239 265
FT      TRANSMEM 266 285
FT      TRANSMEM 286 303
FT      TRANSMEM 304 328
FT      TRANSMEM 329 373
FT      DISULFD 124 202
FT      CARBOHYD 11 11
FT      CARBOHYD 27 27
FT      CARBOHYD 113 113
FT      CARBOHYD 197 197
SQ      SEQUENCE 373 AA; 42212 MW; 944125E9F4560B83 CRC64;
Query Match 19.0%; Score 351.5; DB 1; Length 373;
Best Local Similarity 27.2%; Pred. No. 1.2e-17;
Matches 91; Conservative 66; Mismatches 143; Indels 35; Gaps 8;
QY 18 MPPELLIVANVLCALNGVNLGCFECHKMKWKSSTVLENLAAADPLMLCIPFRIDYLR 77
DB 54 LEAVYLVEFIIIFELGNSVAIMFVEMHKWGISIVYEMFLADPLFLYTLPLALIFYYN 113
QY 78 RHHMAFGDIPCVAGLETTLAINRAGSIVETLVAAADRYFVVRPHNAVNTISTRVAGIYC 137
DB 114 KIDWIFGDAMCKLQRFIFHVNLYGSLFELTLCISAHNYSGVYVPLKSLGGLKKKNALYYAV 173
QY 138 TLMALVIGTVYLLLENHLVQDET-AVSCESFTMESANGMHDIMQLE-----FEMDL 189
DB 174 LVMLVLYVVAISPILFEYSGTGRKNKTVTCYD--FTSNDYLSRYFTYSMCTVAMCIPDL 230
QY 190 GIILFCSEFTWVSLRRQDLARQARKKATRFIMVVAIVETICYLP-----SVSARLY 242
DB 231 VILICQYGLIVKAL-IYNDLDNSPLRKRSIYLVIIIVLTFVAVSYIPFHWKTMNLEARD 289
QY 243 FLMTVPSSACD--PSVHGALHTLTSFTYNSMLDPLVYVESSPFPKFNKLTICSLKPK 300
DB 290 F---OTPEKCDNDKRYATAYVTRGICLASINSCVDPLIVFLAGDTFRRLR----- 337
QY 301 QPHSKTORPEEMPISNLGRCSISVANSFOSOD 335
DB 338 --ATRKASRSEANLQSKSEMTLNLISFEKNGD 370

```

FT	DISTRTD	111	188	BY SIMILARITY.
FT	CARBOHYD	15	15	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	24	24	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	28	28	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	192	192	F -> L (IN REF. 3).
SQ	SEQUENCE	370 AA;	41895 MW;	20857E52A3929E48 CRC64;
Query Match				
Best Local Similarity		18.7%; Score 346.5; DB 1; Length 370;		
Matches 95; Conservative		31.2%; Pred. No. 2.5e-17;		
		52; Mismatches 128; Indels 29; Gaps 11;		
QY	24 VAFVILGALNGVALGCGFEHMKTKPSTVYLLNLAVADFLIMICLPFRDYLRRRRHAF	83		
DB	48 VVFILGILTNSSLSLFPFCFRMKRSETAFTITNLAVSDLEFVCLTPEFI -FYENRHWPF	106		
QY	84 GDIPRCVGLFTLTMNRAGSIVFLVVAADRRFYKVPVHPHAAVNTISTRVAGIVCT-LMAL	142		
DB	107 GDTLCKISGTFALFTNYGSMFLFTICISVDRELAIVYPPRS -RTIIRNSAIVCAGVWL	165		
QY	143 VILGIVYLLLENHLCVQGTAVSC -ESFIMESANGHDMFOLE-----FPMPIGILTF	194		
DB	166 VLSGSIASLSLSTTNVNNATTTCFCGF--SKRWKTYLSKTIPIEVVGFITPLILNVS	222		
QY	195 CSFKIVSLRRRQOLAR-QARRKKATREFIVVAIVFTCYLPSVARSARLYFLMTVPSAC-	252		
DB	223 CSSVYLFTLRKPAFLSQIGTKKKKVLKITVHMAVEVVCAPYNS -VLFLYALVRSGAI	280		
QY	253 -----DPSVHGAHLHTLSFTYMNMSLDLVYVFSSPSPK -FYNLKLCISLKPQGGSK	306		
DB	281 TNCFLERPAKIMYPITTLCLATLNCCEPDFIYFTLESFQSKSYINAHF-----RMESLFR	335		
QY	307 TORP 310			
DB	336 TETP 339			
RESULT 14				
P2Y5_CHICK				
ID	P2Y5_CHICK	STANDARD;	PRT;	308 AA.
AC	P32250;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	P2Y purinoceptor 5 (P2Y5) (Putnergic receptor 5) (6H1).			
GN	P2RY5.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=T-cell;			
RX	MEDLINE=93329058; PubMed=8393036;			
RA	Kaplan M.H., Smith D.I., Sundick R.S.;			
RT	"Identification of a G protein coupled receptor induced in activated			
RT	T cells."			
RL	J. Immunol. 151:628-636(1993).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL	L06109; AAB0587.1; -.			
RR	HSSP; P34996; IDDD.			

QY 184 EEFMPGLILECSFKIWSLRRQOLARQRMK-KATRFIMVVAIVFTCYLP-SYSARL 241
 Db 228 AFTEPFITVWYCYLLIIRSL-RQGLRVERKLTAKAVRMALIVLAFVCPVYHNRSV 285
 QY 242 YFL-WYVSSACDPSYHGL-HITLSFTYMNMDPLVYFSSPSFPKFYNKIKICSLK 298
 Db 286 YVLHYNHSHGASCATORILALANRITSLTSLNGALDPIWFFVAEKFRAHALCNL-LCGKR 344
 QY 299 PKOPGHSKTQPREEMPIS 316
 Db 345 LKGPSPSEKGTNESSLS 362

Search completed: March 26, 2003, 19:38:05
 Job time : 27 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 19:35:13 ; Search time 34 Seconds
(without alignments)
2096.832 Million cell updates/sec

Title: US-09-942-374-2

Perfect score: 1853
Sequence: 1 MYNSCRIEGDTISQVMP.....ANSFOSQSDGOWPHIVEMH 346

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	4 Q9BXC0	Q9BXC0 homo sapien
2	883.5	47.7	363	4 Q8TDS4	Q8TDS4 homo sapien
3	868.5	46.9	360	11 Q9EP66	Q9EP66 mus musculu
4	529	28.5	423	4 Q8TDS5	Q8TDS5 homo sapien
5	450.5	24.3	319	4 Q9NQ20	Q9NQ20 homo sapien
6	446.5	24.1	319	11 Q9JL51	Q9JL51 mus musculu
7	375.5	20.3	309	11 Q8R528	Q8R528 mus musculu
8	351.5	19.0	390	13 Q8Q6Q4	Q8Q6Q4 carassius a
9	342.5	18.5	357	13 Q9DE05	Q9DE05 raja erinac
10	341	18.4	361	13 Q9QX57	Q9QX57 xenopus lae
11	329.5	17.8	380	13 Q9DC06	Q9DC06 carassius a
12	305	16.5	372	4 Q9H1C0	Q9H1C0 homo sapien
13	303.5	16.4	359	6 Q9N0U1	Q9N0U1 ovis aries
14	302.5	16.3	346	4 Q9G6E0	Q9G6E0 homo sapien
15	302.5	16.3	356	4 Q9GTF2	Q9GTF2 homo sapien
16	300.5	16.2	346	6 Q95KS6	Q95KS6 ovis aries

17	299.5	16.2	346	11 Q91Y73	Q91Y73 mus musculu
18	297	16.0	370	13 Q8WU25	Q8WU25 fuqu rubrip
19	297	16.0	399	11 Q8R311	Q8R311 mus musculu
20	293	15.8	315	6 Q9GKP7	Q9GKP7 sus scrofa
21	293	15.8	374	13 Q57466	Q57466 meleagris g
22	293	15.8	385	11 Q9JK40	Q9JK40 mus musculu
23	292.5	15.8	361	6 Q46685	Q46685 bos taurus
24	292	15.8	317	11 Q99MT6	Q99MT6 mus musculu
25	292	15.8	359	6 Q9GLN9	Q9GLN9 pan troglod
26	291.5	15.7	358	4 Q96J28	Q96J28 homo sapien
27	291	15.7	359	11 Q9EPP3	Q9EPP3 cavia porce
28	290.5	15.7	337	4 Q96P68	Q96P68 homo sapien
29	290.5	15.7	359	11 Q99MT7	Q99MT7 mus musculu
30	289	15.6	343	11 Q9QW32	Q9QW32 ratius sp.
31	288.5	15.6	359	11 Q9E0R9	Q9E0R9 meriones un
32	288	15.5	355	11 Q9JUX8	Q9JUX8 ratius norv
33	287.5	15.5	358	11 Q8VE54	Q8VE54 mus musculu
34	287.5	15.5	358	4 Q9BY21	Q9BY21 homo sapien
35	286.5	15.5	355	4 Q9BYX5	Q9BYX5 homo sapien
36	286.5	15.5	423	5 Q964D4	Q964D4 periplaneta
37	286	15.4	359	4 Q8TRK4	Q8TRK4 homo sapien
38	283	15.3	328	11 Q9ERK9	Q9ERK9 mus musculu
39	282.5	15.2	330	4 Q9BXA5	Q9BXA5 homo sapien
40	282.5	15.2	334	4 Q8TDQ8	Q8TDQ8 homo sapien
41	282	15.2	351	6 Q9MXJ9	Q9MXJ9 oryctolagus
42	279	15.1	392	6 Q9BDQ4	Q9BDQ4 canis famill
43	278.5	15.0	355	11 Q91VP9	Q91VP9 mus musculu
44	278.5	15.0	383	13 Q42324	Q42324 catostomus
45	275	14.8	377	13 Q98U14	Q98U14 brachydanio

ALIGNMENTS

RESULT 1
Q9BXC0 PRELIMINARY; PRT; 346 AA.

AC Q9BXC0: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative chemokine receptor (G protein-coupled receptor) (Putative
DE G-protein coupled receptor)
GN FKSG80 OR GPR81 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RT Gene 275:83-91(2001).
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Y.-g, Gong L.;
RT "Molecular cloning of FKSG80, a novel gene encoding a putative
RT chemokine receptor.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF345568; AAK29071.1; -
DR EMBL: AF411110; AAL26481.1; -
DR EMBL: AB083631; BAB89344.1; -
DR HSSP: P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 346 AA; 39295 MW; E0DB14EEB3A47A5 CRC64;

Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1,1e-174;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGSCCRLEGDTISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 60
 DB 1 MNGSCCRLEGDTISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 60
 QY 61 DFLMCLCPFRDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 120
 DB 61 DFLMCLCPFRDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 120
 QY 121 HHAVENTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 180
 DB 121 HHAVENTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 180
 QY 181 FOLEFMPGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 240
 DB 181 FOLEFMPGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 240
 QY 241 LYELMTVPSSACDPVSHGALHITLFTYNNMSMDPLVYFSSPFPKFNKLKISLKR 300
 DB 241 LYELMTVPSSACDPVSHGALHITLFTYNNMSMDPLVYFSSPFPKFNKLKISLKR 300
 QY 301 QPQHSKTQREEMPIISNLGRSCISVANSFOSQSDQMPHIVEMH 346
 DB 301 QPQHSKTQREEMPIISNLGRSCISVANSFOSQSDQMPHIVEMH 346

RESULT 2

Q8RDS4 PRELIMINARY; PRT; 363 AA.

AC Q8RDS4; 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative G-protein coupled receptor.
 GN GPCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT Identification of G protein-coupled receptor genes from the human
 RT genome sequence.";
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB083632; BAB89345.1; -;
 KW Receptor.
 SQ SEQUENCE 363 AA; 41849 MW; CAB0EBC9CCB81D56 CRC64;

Query Match 47.7%; Score 883.5; DB 4; Length 363;
 Best Local Similarity 52.8%; Pred. No. 6e-79;
 Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;

QY 5 SCCRIGDITISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 64
 DB 5 SCCRIGDITISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 64
 QY 17 NCCVDFDIFVILKPLVLEFLFGLGNGLALMIFCFHLKGMKSSRIFFLMLAADELL 76
 DB 17 NCCVDFDIFVILKPLVLEFLFGLGNGLALMIFCFHLKGMKSSRIFFLMLAADELL 76
 QY 65 MCLPRTDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 124
 DB 65 MCLPRTDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 124
 QY 77 IICLPFLMNVYFRMDKMGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 136
 DB 77 IICLPFLMNVYFRMDKMGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 136
 QY 125 NTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 184
 DB 125 NTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 184

DB 137 NKISNRTAAISCLLWITIGLTVHLLKKMPIONGANGILCSSFICHTQEWHEAMFILE 196
 QY 185 FEMPLGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 244
 DB 185 FEMPLGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 244
 DB 197 FFLPGLITLFCFSARILNSLRQ-OMDRHAKKRAITITIMVAIVFTICVLSVSAR 255
 QY 245 WTVPSA--CD--PSVGHALHITLFTYNNMSMDPLVYFSSPFPKFNKLKISLKR 299
 DB 245 WTVPSA--CD--PSVGHALHITLFTYNNMSMDPLVYFSSPFPKFNKLKISLKR 299
 QY 300 KQPHSKTQREEMPIISNLGRSCISVANSFOSQSDQMPHIVEMH 340
 DB 300 KQPHSKTQREEMPIISNLGRSCISVANSFOSQSDQMPHIVEMH 340

RESULT 3

Q9EP66 PRELIMINARY; PRT; 360 AA.

AC Q9EP66; 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Putative seven transmembrane spanning receptor.
 GN PUMA-G.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ, AND C57BL/6;
 RA Schaub A., Pfeiffer K.;
 RT "PUMA-G, an interferon-gamma inducible gene in macrophages is a novel
 RT member of the seven transmembrane spanning superfamily.";
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AJ300199; CAC17791.1; -;
 DR EMBL; AJ300198; CAC17790.1; -;
 DR HSSP; P34996; 1DDD.
 DR MGD; MGI:193383; Puma-g.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF000237; GPCRHHODOPSN.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 360 AA; 41400 MW; CCCES2A2475777FC CRC64;

Query Match 46.9%; Score 868.5; DB 11; Length 360;
 Best Local Similarity 55.6%; Pred. No. 1.8e-77;
 Matches 178; Conservative 39; Mismatches 96; Indels 7; Gaps 4;

QY 3 NG-SCCRIGDITISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 61
 DB 3 NG-SCCRIGDITISQVMPPLIVAFVIALGNGVALCGFCFHKMTWKSTVYLLENLAVA 61
 QY 11 NGKNCVFRDENIAKVPVIGLEFVGLGNGLALMIFCFHLKGMKSSRIFFLMLAA 70
 DB 11 NGKNCVFRDENIAKVPVIGLEFVGLGNGLALMIFCFHLKGMKSSRIFFLMLAA 70
 QY 62 FLMLCLCPFRDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 121
 DB 62 FLMLCLCPFRDYLYRRRRMAFGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 121
 QY 71 FLITICLPFLTDNVVHNMKMGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 130
 DB 71 FLITICLPFLTDNVVHNMKMGDIPCRVGLFTLLAMNAGSIIVFTLVAAADRYKVHP 130
 QY 122 HAVNTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 181
 DB 122 HAVNTSTRVAGIVCTMALVILGTVYLLLENHLCVOETAVSCSEFTMESANGHDI 181
 QY 182 QLEFMPGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 241
 DB 182 QLEFMPGILFCSFKIWSLRROQLARQARKKATRTIMVAIVFTICVLSVSAR 241
 QY 191 LLEFPLALILFCSGRIWSLRQ-OMDRHAKKRAITITIMVAIVFTICVLSVA 249
 DB 191 LLEFPLALILFCSGRIWSLRQ-OMDRHAKKRAITITIMVAIVFTICVLSVA 249
 QY 242 YFLMTVPS--SACD--PSVGHALHITLFTYNNMSMDPLVYFSSPFPKFNKLKIS 296
 DB 242 YFLMTVPS--SACD--PSVGHALHITLFTYNNMSMDPLVYFSSPFPKFNKLKIS 296
 QY 250 RIFMLIKYVNRCDIYSSVDLAFTLLSTYNNMSMDPLVYFSSPFPFSTCINRC 309
 DB 250 RIFMLIKYVNRCDIYSSVDLAFTLLSTYNNMSMDPLVYFSSPFPFSTCINRC 309

OY 297 LKPGHSGKTOPPEEMPS 316
 Db 310 LKRTIGEPDNNRSTSELT 329

RESULT 4

O8TDS5

ID 08TDS5 PRELIMINARY; PRT: 423 AA.

AC 08TDS5: 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)

GN Putative G-protein coupled receptor.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Takeda S., Kadowaki S., Haga T., Takasu H., Mitaku S.,
 RT Identification of G protein-coupled receptor genes from the human
 genome sequence.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB083630; BAB89343.1; -

KW Receptor.

SQ SEQUENCE 423 AA; 45810 MW; 72ADA9F43A9EC051 CRC64;

Query Match

Best Local Similarity 28.5%; Score 529; DB 4; Length 423;

Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps 7;

OY 4 GSCRIEGDTISQVMPPLIYAVLGAALGNGVALCGFCFHKMTWKSTYVLEMLVADFL 63
 Db 81 GPCHTSSSLVSAFLAPITALEFLVGLVGNLSALFTFCHTRTWTSNTVFLVLADEL 140
 OY 64 LMICLPRTDYLLRRHMAFGDIPRCVGLFTLMMNRAGSIVFTVVAADRYFVHPHNA 123
 Db 141 LISNPLRDYVYLHETWRGAACKYNLFMLSTNKTASVFLTALANRYLKVPVPHV 200
 OY 124 VNTISRVAGIVCTIMALVILGTVYLLLENHLCVQE-TAVSCSEFTM---ESANGWHD 178
 Db 201 LSRASVGAARVAGLWVGI-----LLNGHLLSTFSGPSCLSYRVGKPSASLRMQ 254
 OY 179 IMQLEFEMFGLITFCSEFKIWSLRROQLARQAKKATRFIMVAIVETICYPSV- 237
 Db 255 ALYLLEFPLALILEFAIVSIGLITRRR-GLGQAGPQARMRLVAVVAVYTICFLPSII 313
 OY 238 --SARLFTLVTPSSA---CDPSVHGALHTLSTFTYNSMLADLVYFFSSPSF 285
 Db 314 FGMAWMAFPLMSACRSRLDCTQLFHG---SLAFYTLNSVLDVLCFSSPNF 362

RESULT 5

O9N020

ID 09N020 PRELIMINARY; PRT: 319 AA.

AC 09N020: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

GN BA517H2.2 (G protein-coupled receptor 31).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Almeida J.,

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL121935; CAB99329.1; -

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 319 AA; 35074 MW; 2ACD0350AD/FB53A CRC64;

Query Match

Best Local Similarity 24.3%; Score 450.5; DB 4; Length 319;

Matches 101; Conservative 61; Mismatches 121; Indels 11; Gaps 5;

OY 7 CRIGEDTISQVMPPLIYAVLGAALGNGVALCGFCFHKMTWKSTYVLEMLVADFLMI 66
 Db 6 CSAPSTVATAGVILGECGLIGLGNALMTFLFVRYKPAVYVLTALADLLIAA 65
 OY 67 CLPFTDYLLRRHMAFGDIPRCVGLFTLMMNRAGSIVFTVVAADRYFVHPHNAVNT 126
 Db 66 CLPFLAAYLLSLQAAHNLRCVGMALHFLDLSRSGMFLAAVADRLRVVHPRKLVNL 125
 OY 127 ISTRVAGIVCTIMALVILGTVYLLLENHLCVQE-TAVSCSEFTMANG---WHDIMF 181
 Db 126 LSPQALAGVSGVLMWLMALTCPGLLISE--AAQNSTGCHSF-YSRADGSFIIHQEALS 182
 OY 182 QLEFPMPLGITLFCSEFKIWSLRRL-QOLARQAKKATRFIMVAIVETICYPSVARS 240
 Db 183 CLQFVLPGLIVFCNAGIIRALQKRLREPERKQPLQRAQALVTIVLVFALCFPLCELAR 242
 OY 241 --LYFLWVPPSSACDPSVHGALHTLSTFTYNSMLADLVYFFSSPSFKEYNKL 292
 Db 243 VLMHIFQNLGSCRALCAVAHNSDVGLTLYLSVLPVAVYCPSSPFRSSYRV 296

RESULT 6

O9JL51

ID 09JL51 PRELIMINARY; PRT: 319 AA.

AC 09JL51: 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)

GN G protein coupled receptor.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99431663; PubMed-10501965;

RA Schimenti J.C.;

RT "ORPless, intronless, and mutant transcription units in the mouse t

RL complex responder (tcr) locus.";

EMBL; AF140708; AAF26668.1; -

MGD; MGI:98543; Tcrp10c.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCR_RHODPSN.

DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.

KW Receptor.

SQ SEQUENCE 319 AA; 35551 MW; 571F6DFB485BD7C4 CRC64;

Query Match

Best Local Similarity 24.1%; Score 446.5; DB 11; Length 319;

Matches 104; Conservative 64; Mismatches 133; Indels 19; Gaps 7;

OY 7 CRIGEDTISQVMPPLIYAVLGAALGNGVALCGFCFHKMTWKSTYVLEMLVADFLMI 66
 Db 6 CSASTVETAGVTLTLCVILGIMGNVALTFFRYLKVMPVAVYVLTALADLLIAT 65
 OY 67 CLPFTDYLLRRHMAFGDIPRCVGLFTLMMNRAGSIVFTVVAADRYFVHPHNAVNT 126
 Db 66 SVFFAAYLKGTWKLGIMPCQLLFLTAFSCGVGVAFMLTVALDRYLVVHPRKLVNL 125

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QY 127 ISTRAAAVICTWALVILGVYLLLEHNLIC-VOETAAVCSGSPF-----MSAANGWHIME 181
Dp 126 LSTRAAWISSILIMLIMAVVLPOLL---TCRTTQNSIECSFEPPTGGTKAIATQDEVLF 182
QY 182 QLEPFPYGIILFCSFKIWSLRRLR-OOLARQAMKRAKTRFIMVAVIVFTCYLPYSAR 240
Dp 183 FLQVLLPFGILISFCNSGILFTLQKRLSDSKQPTIRARVAVLAIMLLLFGLCFELPSVLR 242
QY 241 --LVELWVPSACDPVHGALHLLTSFTYNSMLDPLVYIFSSPSPKPFYKNIKICSLK 298
Dp 243 VLVNHFQEFKCSQVOQALMRASDIAGSLTCLHSLSPAIYCFSNPATFHSRYK-LKSLR 301
QY 299 PKQFCHSKTORPEMPISNL 318
Dp 302 GR-----KKAESPSPDNL 314

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RESULT 7			
08R528			
ID	08R528	PRELIMINARY;	PRT; 309 AA.
AC	08R528;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Cysteiny[leukotriene 2 receptor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Usnil S.;		
RT	"Mouse CysLT2 Gene.";		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB058930; BAB86881.1; -		
KW	Receptor.		
SO	SEQUENCE	309 AA;	35226 MW; 06FACCB8AF96574 CRC64;

Query Match	20.3%	Score 375.5:	DB 11:	length 309:
Best Local Similarity	32.7%	Pred. No. 75-29:		
Matches	96:	Conservative	56:	Mismatches 125: Indels 17: Gaps 7
QY	2	YNOSCCRIBSDITISQVMPPLLIVAFVGLANGVALGCFCEHMTWKPRST--	YLYFNLA	58
Db	10	YSNRNCTIE--NFKREYPIITVILIFFWGALNGSEIYVF--LQTKCKSTSVNFMENLA	65	
QY	59	VAFELLMICLPFRDYVYLRRRHMAFGDIPCRGFLFTLMNRAGSIIVFLTYAADREKYV	118	
Db	66	TSDFLEITSLPFRADYDFRGSNMITGDLACRMASTSLVNNYNTISITFLTYLSVYRELATY	125	
QY	119	HPHHAVNTISTRYAGICTVCTLMALVILGTVYLLIENHLQVETAVSC---ESFIMESA	173	
Db	126	HPRFMFHYVTSVR--SAWILGIIIVFIMASALLVNGOEBEEDNITISCELSPOKF--KSL	182	
QY	174	NGCHMDIFOLFEPMPGIIIFCSFKIVMSLRRO--QLARQRKMKDRFLMVAVYET	231	
Db	183	LIMNHIAVAVGFLPRLPLTITCYLLILILKLKAEIPESGPAARKKALLTIVIAMITFEL	242	
QY	232	CYIPSVSARILFLWYVPSACDPVSHGALHTLSFTYNSMLDPLVYFSSPSE	285	
Db	243	CFLPYHALRTLHLVYWDKDCGDVLRHKATVITLTMAAANSCFNELFYFAGENE	296	
RESULT 8				
AC	080G04	PRELIMINARY:	PRT:	390 AA.
DT	01-JUN-2002	(TREMBlrel. 21, Created)		
DT	01-JUN-2002	(TREMBlrel. 21, last sequence update)		
DT	01-JUN-2002	(TREMBlrel. 21, last annotation update)		
DE	Type five-like somatostatin receptor.			
OS	Carassius auratus (Goldfish).			
QC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC Actinopterygii: Neopterygii: Teleostei: Ostariophysi: Cypriniformes:
 CC Cyprinidae: Carassius.
 RX NCBI_TaxID=7957;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Lin X., Peter R.E.;
 RT "Cloning and expression of a type five somatostatin receptor in
 RT goldfish.";
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF252879; AM18805.1; -
 KW Receptor.
 SQ SEQUENCE 390 AA: 44136 MW: EC12119A4B6CF9A8 CRC64;

[illegible]

RESULT	9
Q9DE05	PRELIMINARY; PRT; 357 AA.
AC	Q9DE05;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	P2y receptor.
OS	Raja erinacea (Little skate).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes
OC	Elasmobranchii; Squalae; Hyposqualae; Pristiogadidae; Batoidae;
OC	Rajiformes; Rajidae; Raja.
OX	NCBI_TaxID=7782;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER;
RX	MEDLINE=20459151; PubMed=10900200;
RA	Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.
RA	Ballatori N., Boyer J.L., Nathanson M.H.,
RT	"A primitive ATP receptor from the little skate <i>Raja erinacea</i> .";
RL	J. Biol. Chem. 275:30701-30706(2000).
EMBL	AF242850; AAG42684.1; "
DR	HSSP; P34996; 1DDO.
DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm_1.1.
DR	PRINTS; PRO023; GPCRHHODOPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
KM	Receptor.
QO	SEQUENCE 357 AA; 41239 MW; 14604DE15DCBD941 CRC64;


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DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative G protein-coupled receptor 92 (Putative G-protein coupled
DE receptor).
GN GPR92 OR GPR93 OR GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
RA Lorenz-Depierreux B., Grabowski M., Meitinger T., Strom T.M.,
RA "Autosomal dominant hypophosphataemic rickets is associated with
RA mutations in FGFR3."
RT Nat. Genet. 26:345-348(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Atkilitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RA "Discovery and mapping of ten novel G protein-coupled receptor
RA genes."
RT Gene 275:83-91(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence."
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ272207; CAC03725.1;
DR EMBL: AF411112; ALN26483.1;
DR EMBL: AB083600; BAB9313.1;
DR HSSP: P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 372 AA; 41346 MW; BA35709084BB6D84 CRC64;

Query Match 16.5%; Score 305; DB 4; Length 372;
Best Local Similarity 29.4%; Pred. No. 7.8e-22;
Matches 91; Conservative 44; Mismatches 125; Indels 50; Gaps 10;

QY 13 TISQVMP-----PLLIYAFVLAGAIG--NGVALCGCFCHMKTKPSTVYLFINAV 59
DB 8 TNSVSLPCPDYRPTFRHLRLVYSLVLA-GRLNALMLVLRALRVHSHVSVTMCNLLA 66
QY 60 ADELMLICLPRTDYLLRRHMAFGDIPCRVGLFTLANRAGSIVFTLVVAADRYFVVH 119
DB 67 SDLFTLSLPVRLSY-ALHHMPFDLLCQTGAIFQNMVSGSCIFMLINVDYALIVH 125
QY 120 PHNAVNTSTRAAGIVCTMALVITGV-----YLLLENHLCVQETAVSCS 167
DB 126 PLRLHRLRRPVARALICGVALLIVAVPARVHRPSRCYRDLERVLGCF-----ES 178
QY 168 FIMESANGMHDIMF-----OLEEFMPLGILFCSPKIYWSLRRQOLARQARKKATR 220
DB 179 F---SDELMKGRLLPLVLLALGFLPLPLAVVYSSGVTFETLARPRATQSQ-RRKTVR 234
QY 221 FIMVVAIVITCYLP-----SVSARLYFLMTVPSSACDPVHGALHTLTSFTYNSMLDP 275
DB 235 LLNLNVLFLCFLVYNTSLAVVGLRSKIVAAVSPARDVRGVLMVLLAGANCVLDP 294
QY 276 LVYFSSPSF 285
DB 295 LVYFSAEGF 304

RESULT 13
Q9N001 PRELIMINARY; PRT; 359 AA.
AC Q9N001;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Angiotensin II type 1 receptor.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=ADRENAL CORTEX;
RA Bird I.M., Milligan D.S.;
RT "Isolation of a full length ovine Angiotensin II Type-1 Receptor (AT1-
RT R) cDNA."
RL Endocr. Res. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF254119; AAF6063.1;
DR HSSP: P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41062 MW; C07010EDB8110EB CRC64;

Query Match 16.4%; Score 303.5; DB 6; Length 359;
Best Local Similarity 24.9%; Pred. No. 1.1e-21;
Matches 81; Conservative 68; Mismatches 143; Indels 33; Gaps 8;

QY 17 VMPDLIVAFVLAGALGVALCGCFCHMKTKPSTVYLFINAVADFLMICLPFTDYLL 76
DB 30 MIPLYIIFVVGIFGFSNIVIVFYMKLKVAVSVELLNLADCFLLTLPIMAVITA 89
QY 77 RRRHMAFGDIPCRVGLFTLANRAGSIVFTLVVAADRYFVVHPHNAVNTSTRAAGIV 136
DB 90 MEYRMPRGNTLCKIAGSVSEFNLYASVFLTCLSIDRYALIVPMKS-RLRRTMLAKYV 148
QY 137 C-TLMAVILITGVYLL-ENHLCVQETAVSCSFIMESANGMHDIMFOLE-----FEMPL 189
DB 149 CLIIWLLAGLASLPTIIHRVFEIENTNITVCAFHYESQSTLPVGLTKNIIQFLPE 208
QY 190 GILFCSPKIYWSLRRQOLARQARKKATRELMVAIV-FITCYLP-----SVSARLYF 243
DB 209 -LIIITSYTLIMTKLRAVEIQNKRPKDDIFKILAIIVLEFFESVWPHQIFMDVILQ 267
QY 244 LMTVPSSACDPVHGALHTLTSFTYNSMLDPLVYFESSPPKRY----- 289
DB 268 LGILIRCKIEDIVDMPTTICLAFNNCLNPLFGLGKKKKYFLDLKXIPKAKSH 327
QY 290 ----NLIKISLKPQKQSHKTOPR 310
DB 328 SNLSTKMSLTLSYRPSNGNSSTKKP 352

RESULT 14
Q9G6E0 PRELIMINARY; PRT; 346 AA.
AC Q9G6E0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:3354783) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EYE;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009522; AA009522.1;
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
 FT NON_TER
 SQ SEQUENCE 346 AA; 38790 MW; EA073A6CC05FEEB72 CRC64;

Query Match 16.3%; Score 302.5; DB 4; Length 346;
 Best Local Similarity 29.8%; Pred. No. 1.3e-21;
 Matches 90; Conservative 50; Mismatches 135; Indels 27; Gaps 9;

QY 13 TISQVMPPLLIYAVFVGLGNGVALGCFCHMKTKPSTVYLLENLAVADFLMICLPRT 72
 Db 18 TSNVLTFTFYVVCIIIGLGNLTIVYILIRYAKMTITINILALADELFMLGLPFLA 77
 QY 73 DYLLRRRHMAFGDIPCRVGLFTLAMNRAGSIYFLTVVADRYEKVYHPHHAVNTISTRYA 132
 Db 78 -MQVALVHMPFGKALGRVYMTVDGINQFTSIFCLTVMSIDRLAVVHPKSAKRRPRTA 136
 QY 133 AGIVCTLMA---LVILG-TVYLLLENHLCVQETAVSCSEFIMESANGWHD---IMFOLE 184
 Db 137 KMITMAVGVSLVILPIIMIVAGLRSN---QWGRSSCTIMWPEGSGAWYTGFIITYFTILG 193
 QY 185 FEMPLGIILFCSEFKIYWSLR---RRQQLARQARKKATRFIMVVAIVETICYLPSVSAR 240
 Db 194 FLVPLTIILCYLFIITIKKSSGIRVSSKRRKSEKKTVMVIVAVVIFCWLDP----- 248
 QY 241 LYFLMTVPSSAC---DPSVHGALHITLSTFYNNMSMDPLVYVYFSSPSPKPKYNNKLTICS 296
 Db 249 -FYIFNVSSVSMASIPTPALKGMDFEVVYLTITANSCANPIIYAFILSDNFKKSFQNV-LCL 306
 QY 297 LK 298
 Db 307 VK 308

RESULT 15
 Q96TF2 PRELIMINARY; PRT; 356 AA.
 AC Q96TF2;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Somatostatin receptor 2B.
 GN SSTR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20084417; PubMed=10619399;
 RA Petersen S., Rasch A.C., Presch S., Bell F.U., Schulte H.M.;
 RT Genomic structure and transcriptional regulation of the human
 RT somatostatin receptor type 2.
 RL Mol. Cell. Endocrinol. 157:75-85(1999).
 DR EMBL: AF184174; AAF42810.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_FL2; 1.
 SQ SEQUENCE 356 AA; 40006 MW; D10FA237FED61F3 CRC64;

Query Match 16.3%; Score 302.5; DB 4; Length 356;
 Best Local Similarity 29.8%; Pred. No. 1.3e-21;
 Matches 90; Conservative 50; Mismatches 135; Indels 27; Gaps 9;

QY 13 TISQVMPPLLIYAVFVGLGNGVALGCFCHMKTKPSTVYLLENLAVADFLMICLPRT 72
 Db 41 TSNVLTFTFYVVCIIIGLGNLTIVYILIRYAKMTITINILALADELFMLGLPFLA 100
 QY 73 DYLLRRRHMAFGDIPCRVGLFTLAMNRAGSIYFLTVVADRYEKVYHPHHAVNTISTRYA 132
 Db 101 -MQVALVHMPFGKALGRVYMTVDGINQFTSIFCLTVMSIDRLAVVHPKSAKRRPRTA 159
 QY 133 AGIVCTLMA---LVILG-TVYLLLENHLCVQETAVSCSEFIMESANGWHD---IMFOLE 184
 Db 160 KMITMAVGVSLVILPIIMIVAGLRSN---QWGRSSCTIMWPEGSGAWYTGFIITYFTILG 216
 QY 185 FEMPLGIILFCSEFKIYWSLR---RRQQLARQARKKATRFIMVVAIVETICYLPSVSAR 240
 Db 217 FLVPLTIILCYLFIITIKKSSGIRVSSKRRKSEKKTVMVIVAVVIFCWLDP----- 271
 QY 241 LYFLMTVPSSAC---DPSVHGALHITLSTFYNNMSMDPLVYVYFSSPSPKPKYNNKLTICS 296
 Db 272 -FYIFNVSSVSMASIPTPALKGMDFEVVYLTITANSCANPIIYAFILSDNFKKSFQNV-LCL 329
 QY 297 LK 298
 Db 330 VK 331

Search completed: March 26, 2003, 19:38:47
 Job time : 37 secs

